

SEP 16 2000

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Recombinant Biocatalysis, Inc.
(ii) TITLE OF INVENTION: THERMOSTABLE PHOSPHATASES
(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows 95
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US97/10784
(B) FILING DATE: 19-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/666,857
(B) FILING DATE: 19-JUN-1996

- (A) APPLICATION NUMBER: 60/033,752
(B) FILING DATE: 19-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Haile, Ph.D., Lisa A.
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 09010/015W01

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619/678-5070
(B) TELEFAX: 619/678-5099
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGGGGCA GTCCGAAAA GG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 CCGAGGATCC TCACCGCCCC CTGCGGGTGC G 31

 (2) INFORMATION FOR SEQ ID NO:3:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGTTGGAT ATACTGCTTG TT 52

 (2) INFORMATION FOR SEQ ID NO:4:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 CCGACGATCC TTATTTTTTA ACCAAATGTT CC 32

 (2) INFORMATION FOR SEQ ID NO:5:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 CCGACAATG ATTAAAGAGG AGAAATTAAC TATGATGATG GAATTCATC GC 52

 (2) INFORMATION FOR SEQ ID NO:6:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 CCGAGGATCC CTACAGTTCT AAAAGTCTTT TA 32

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGAGAACC CTGACAATAA AC

52

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAGGATCC TTACACCCAC AGAACCTTA C

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAAAGGA AAGTCTCTTG TT

52

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGAGGATCC TCAAGCTTCC TGGAGAATCA A

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGCCAAGA AATATCGCCG CT

52

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGAGGATCC TTAAGGCTTC TCGAGGTGGG GGTT

34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTATAAA TGGATTATTG AGGG

54

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGAGGACTA AACATAGTCT AAGTAATTAG C

31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGAGAATC CTCCTCACCA AC

52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGAGGATCC TCACAGGCTC AGAAGCCTTT G

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGAGAATTC ATTAAAGAGG AGAAATTAAC TATGGAAAAC TTAAAAAAGT ACCT

54

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGAGGATCC TCACCGCCCC CTGCGGGTGC G

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG AGG GGG AGC GGA GTG CGG ATA CTT CTC ACC AAC GAT GAC GGC ATC
Met Arg Gly Ser Gly Val Arg Ile Leu Leu Thr Asn Asp Asp Gly Ile
1 5 10 15

48

TTT GCC GAG GGT CTG GGG GCT CTG CGC AAG ATG CTG GAG CCC GTG GCT
Phe Ala Glu Gly Leu Gly Ala Leu Arg Lys Met Leu Glu Pro Val Ala
20 25 30

96

ACC CTT TAC GTG GTG GCT CCG GAC CGA GAG CGT AGC GCG GCC AGC CAT
Thr Leu Tyr Val Val Ala Pro Asp Arg Glu Arg Ser Ala Ala Ser His

144

35	40	45	
GCT ATC ACC GTT CAC CGC CCC CTG CGG GTG CGG GAG GCG GGT TTT CGC			192
Ala Ile Thr Val His Arg Pro Leu Arg Val Arg Glu Ala Gly Phe Arg			
50 55 60			
AGC CCC AGG CTT AAA GGC TGG GTA GTG GAC GGT ACC CCG GCC GAC TGC			240
Ser Pro Arg Leu Lys Gly Trp Val Val Asp Gly Thr Pro Ala Asp Cys			
65 70 75 80			
GTC AAG CTG GGC CTG GAG GTA CTT TTG CCC GAA CGT CCA GAT TTC CTG			288
Val Lys Leu Gly Leu Glu Val Leu Leu Pro Glu Arg Pro Asp Phe Leu			
85 90 95			
GTT TCG GGC ATA AAC TAC GGG CCC AAC CTG GGT ACC GAC GTA CTT TAC			336
Val Ser Gly Ile Asn Tyr Gly Pro Asn Leu Gly Thr Asp Val Leu Tyr			
100 105 110			
TCC GGC ACC GTC TCG GCG GCC ATA GAA GGG GTA ATT AAC GGC ATT CCC			384
Ser Gly Thr Val Ser Ala Ala Ile Glu Gly Val Ile Asn Gly Ile Pro			
115 120 125			
TCG GTG GCC GTA TCT TTG GCC ACG CGG CGG GAG CCG GAC TAT ACC TGG			432
Ser Val Ala Val Ser Leu Ala Thr Arg Arg Glu Pro Asp Tyr Thr Trp			
130 135 140			
GCG GCC CGG TTC GTC CTG GTC CTG CTG GAG GAA CTG CGA AAA CAC CAA			480
Ala Ala Arg Phe Val Leu Val Leu Leu Glu Glu Leu Arg Lys His Gln			
145 150 155 160			
CTG CCC CCA GGA ACC CTG CTC AAC GTC AAC GTG CCC GAC GGG GTG CCC			528
Leu Pro Pro Gly Thr Leu Leu Asn Val Asn Val Pro Asp Gly Val Pro			
165 170 175			
CGC GGG GTC AAG GTG ACC AAA CTG GGA AGC GTA CGC TAC GTC AAC GTG			576
Arg Gly Val Lys Val Thr Lys Leu Gly Ser Val Arg Tyr Val Asn Val			
180 185 190			
GTA GAC TGC CGC ACC GAC CCT CGG GGG AAG GCT TAC TAC TGG ATG GCG			624
Val Asp Cys Arg Thr Asp Pro Arg Gly Lys Ala Tyr Tyr Trp Met Ala			
195 200 205			
GGA GAA CCA TTG GAG CTG GAC GGC AAC GAC TCC GAA ACC GAC GTC TGG			672
Gly Glu Pro Leu Glu Leu Asp Gly Asn Asp Ser Glu Thr Asp Val Trp			
210 215 220			
GCG GTG CGA GAA GGC TAT ATT TCC GTA ACA CCG GTC CAG ATC GAC CTT			720
Ala Val Arg Glu Gly Tyr Ile Ser Val Thr Pro Val Gln Ile Asp Leu			
225 230 235 240			
ACT AAC TAC GGC TTC CTG GAA GAA CTC AAA AAA TGG CGT TTC AAG GAT			768
Thr Asn Tyr Gly Phe Leu Glu Glu Leu Lys Lys Trp Arg Phe Lys Asp			
245 250 255			
ATC TTT TCT TCT TAA			783
Ile Phe Ser Ser			
260			

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG TTG GAT ATA CTG CTT GTT AAT GAT GAT GGC ATT TAT TCA AAT GGA	48
Met Leu Asp Ile Leu Leu Val Asn Asp Asp Gly Ile Tyr Ser Asn Gly	
1 5 10 15	
TTA ATA GCT TTG AAG GAT GCA TTA TTG GAA AAA TTT AAT GCG AGG ATT	96
Leu Ile Ala Leu Lys Asp Ala Leu Leu Glu Lys Phe Asn Ala Arg Ile	
20 25 30	
ACT ATT GTA GCC CCA ACA AAT CAG CAG AGT GGT ATT GGT AGG GCA ATA	144
Thr Ile Val Ala Pro Thr Asn Gln Gln Ser Gly Ile Gly Arg Ala Ile	
35 40 45	
AGT TTA TTC GAG CCG TTA AGG ATA ACT AAA ACC AAA TTA GCA GAT GGT	192
Ser Leu Phe Glu Pro Leu Arg Ile Thr Lys Thr Lys Leu Ala Asp Gly	
50 55 60	
TCT TGG GGA TAT GCA GTT TCA GGA ACC CCA ACA GAT TGC GTT ATA TTG	240
Ser Trp Gly Tyr Ala Val Ser Gly Thr Pro Thr Asp Cys Val Ile Leu	
65 70 75 80	
GGC ATT TAT GAG ATA TTA AAG AAG GTA CCT GAT GTA GTT ATA TCA GGA	288
Gly Ile Tyr Glu Ile Leu Lys Lys Val Pro Asp Val Val Ile Ser Gly	
85 90 95	
ATA AAC ATT GGA GAA AAC CTT GGG ACT GAA ATA ACA ACT TCT GGA ACG	336
Ile Asn Ile Gly Glu Asn Leu Gly Thr Glu Ile Thr Thr Ser Gly Thr	
100 105 110	
TTG GGG GCT GCG TTT GAA GGG GCC CAT CAT GGG GCT AAG GCA TTA GCA	384
Leu Gly Ala Ala Phe Glu Gly Ala His His Gly Ala Lys Ala Leu Ala	
115 120 125	
TCA TCA CTC CAA GTT ACC TCT GAC CAT CTA AAG TTT AAA GAG GGG GAG	432
Ser Ser Leu Gln Val Thr Ser Asp His Leu Lys Phe Lys Glu Gly Glu	
130 135 140	
ACC CCA ATA GAC TTC ACA GTC CCA GCA AGA ATT ACT GCA AAT GTT GTT	480
Thr Pro Ile Asp Phe Thr Val Pro Ala Arg Ile Thr Ala Asn Val Val	
145 150 155 160	
GAG AAG ATG TTG GAT TAT GAT TTC CCA TGT GAT GTC GTC AAC TTA AAC	528
Glu Lys Met Leu Asp Tyr Asp Phe Pro Cys Asp Val Val Asn Leu Asn	
165 170 175	
ATT CCA GAA GGA GCA ACA GAA AAG ACA CCG ATT GAA ATC ACA AGG TTG	576
Ile Pro Glu Gly Ala Thr Glu Lys Thr Pro Ile Glu Ile Thr Arg Leu	
180 185 190	
GCA AGG AAA ATG TAT ACA ACA CAC GTT GAG GAA AGA ATA GAT CCA AGA	624
Ala Arg Lys Met Tyr Thr Thr His Val Glu Glu Arg Ile Asp Pro Arg	
195 200 205	
GGG AGG AGT TAT TAT TGG ATT GAT GGG TAT CCT ATT TTA GAG GAA GAG	672
Gly Arg Ser Tyr Tyr Trp Ile Asp Gly Tyr Pro Ile Leu Glu Glu Glu	
210 215 220	

GAA GAC ACT GAT GTC TAT GTT GTT AGA AGA AAG GGA CAT ATT TCT CTA	720
Glu Asp Thr Asp Val Tyr Val Val Arg Arg Lys Gly His Ile Ser Leu	
225 230 235 240	
ACC CCA TTA ACA TTA GAC ACA ACA ATT AAA AAT TTA GAG GAA TTT AAG	768
Thr Pro Leu Thr Leu Asp Thr Thr Ile Lys Asn Leu Glu Glu Phe Lys	
245 250 255	
AAA AAA TAT GAG AGA ATA TTA AAT GAA TGA	798
Lys Lys Tyr Glu Arg Ile Leu Asn Glu	
260 265	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG ATG ATG GAA TTC ACT CGC GAG GGA ATA AAA GCT GCT GTA GAG GCA	48
Met Met Met Glu Phe Thr Arg Glu Gly Ile Lys Ala Ala Val Glu Ala	
1 5 10 15	
CTT CAA GGG TTA GGA GAG ATC TAC GTA GTT GCC CCA ATG TTT CAA AGG	96
Leu Gln Gly Leu Gly Glu Ile Tyr Val Val Ala Pro Met Phe Gln Arg	
20 25 30	
AGC GCA AGT GGA AGG GCA ATG ACC ATC CAC AGA CCT CTA AGG GCT AAA	144
Ser Ala Ser Gly Arg Ala Met Thr Ile His Arg Pro Leu Arg Ala Lys	
35 40 45	
AGA ATA AGT ATG AAC GGT GCA AAA GCA GCC TAT GCT TTG GAT GGA ATG	192
Arg Ile Ser Met Asn Gly Ala Lys Ala Ala Tyr Ala Leu Asp Gly Met	
50 55 60	
CCC GTT GAT TGC GTT ATC TTT GCC ATG GCC AGA TTT GGA GAT TTC GAC	240
Pro Val Asp Cys Val Ile Phe Ala Met Ala Arg Phe Gly Asp Phe Asp	
65 70 75 80	
CTT GCA ATA AGT GGT GTA AAC TTG GGA GAA AAC ATG AGC ACC GAG ATA	288
Leu Ala Ile Ser Gly Val Asn Leu Gly Glu Asn Met Ser Thr Glu Ile	
85 90 95	
ACG GTT TCC GGG ACT GCA AGC GCT GCA ATA GAG GCT GCA ACC CAA GAG	336
Thr Val Ser Gly Thr Ala Ser Ala Ala Ile Glu Ala Ala Thr Gln Glu	
100 105 110	
ATC CCA AGC ATT CCC ATA AGC CTG GAA GTT AAT AGA GAA AAA CAC AAA	384
Ile Pro Ser Ile Pro Ile Ser Leu Glu Val Asn Arg Glu Lys His Lys	
115 120 125	
TTT GGT GAG GGC GAA GAG ATT GAC TTC TCA GCT GCC AAG TAT TTC CTA	432
Phe Gly Glu Gly Glu Glu Ile Asp Phe Ser Ala Ala Lys Tyr Phe Leu	
130 135 140	
AGA AAA ATC GCA ACG GCG GTT TTA AAG AGA GGC CTC CCC AAA GGA GTC	480

Arg Lys Ile Ala Thr	Ala Val Leu Lys Arg	Gly Leu Pro Lys Gly Val	
145	150	155	160
GAT ATG CTG AAC GTC AAC GTC CCT TAT GAT GCA AAT GAA AGG ACA GAG			528
Asp Met Leu Asn Val Asn Val Pro Tyr Asp Ala Asn Glu Arg Thr Glu			
	165	170	175
ATA GCT TTT ACT CGC CTG GCA AGA AGG ATG TAT AGG CCT TCT ATT GAA			576
Ile Ala Phe Thr Arg Leu Ala Arg Arg Met Tyr Arg Pro Ser Ile Glu			
	180	185	190
GAG CGC ATA GAC CCA AAG GGG AAT CCC TAC TAC TGG ATA GTT GGA ACT			624
Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr Trp Ile Val Gly Thr			
	195	200	205
CAG TGC CCT AAG GAG GCA TTA GAG CCG GGA ACG GAT ATG TAT GTA GTT			672
Gln Cys Pro Lys Glu Ala Leu Glu Pro Gly Thr Asp Met Tyr Val Val			
	210	215	220
AAA GTT GAG AGA AAA GTT AGC GTG ACT CCA ATA AAC ATT GAT ATG ACA			720
Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile Asp Met Thr			
	225	230	235
GCA AGA GTG AAT TTA GAC GAG ATT AAA AGA CTT TTA GAA CTG			762
Ala Arg Val Asn Leu Asp Glu Ile Lys Arg Leu Leu Glu Leu			
	245	250	
TAG			765

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG AGA ACC CTG ACA ATA AAC ACT GAC GCG GAG GGG TTC GTT TTG AGG			
Met Arg Thr Leu Thr Ile Asn Thr Asp Ala Glu Gly Phe Val Leu Arg			48
1	5	10	15
ATT CTC CTG ACG AAC GAC GAT GGA ATC TAC TCC AAC GGA CTG CGC GCC			96
Ile Leu Leu Thr Asn Asp Asp Gly Ile Tyr Ser Asn Gly Leu Arg Ala			
	20	25	30
GCT GTG AAA GCC CTG AGT GAG CTC GGC GAA GTT TAC GTC GTT GCC CCC			144
Ala Val Lys Ala Leu Ser Glu Leu Gly Glu Val Tyr Val Val Ala Pro			
	35	40	45
CTC TTC CAG AGG AGC GCG AGC GGC AGG GCC ATG ACG CTC CAC AGG CCG			192
Leu Phe Gln Arg Ser Ala Ser Gly Arg Ala Met Thr Leu His Arg Pro			
	50	55	60
ATA AGG GCC AAG CGC GTT GAC GTT CCC GGC GCA AAG ATA GCC TAC GGA			240
Ile Arg Ala Lys Arg Val Asp Val Pro Gly Ala Lys Ile Ala Tyr Gly			
	65	70	75
			80

ATA GAT GGA ACT CCT ACT GAC TGC GTG ATT TTC GCC ATA GCC CGC TTC	288
Ile Asp Gly Thr Pro Thr Asp Cys Val Ile Phe Ala Ile Ala Arg Phe	
85 90 95	
GGG AGC TTT GGT TTA GCC GTG AGC GGG ATT AAC CTC GGC GAG AAC CTG	336
Gly Ser Phe Gly Leu Ala Val Ser Gly Ile Asn Leu Gly Glu Asn Leu	
100 105 110	
AGC ACC GAG ATA ACA GTC TCA GGG ACG GCC TCC GCT GCC ATA GAG GCC	384
Ser Thr Glu Ile Thr Val Ser Gly Thr Ala Ser Ala Ala Ile Glu Ala	
115 120 125	
TCA ACT CAT GGA ATT CCG AGC ATA GCG ATT AGC CTT GAG GTG GAG TGG	432
Ser Thr His Gly Ile Pro Ser Ile Ala Ile Ser Leu Glu Val Glu Trp	
130 135 140	
AAG AAG ACC CTC GGC GAG GGT GAG GGG GTT GAC TTC TCG GTC TCG ACT	480
Lys Lys Thr Leu Gly Glu Gly Glu Val Phe Ser Val Ser Thr	
145 150 155 160	
CAC TTC CTC AAG AGA ATC GCG GGA GCC CTC TTG GAG AGA GGT CTT CCT	528
His Phe Leu Lys Arg Ile Ala Gly Ala Leu Leu Glu Arg Gly Leu Pro	
165 170 175	
GAG GGC GTT GAC ATG CTC AAC GTC AAC GTT CCG AGC GAC GCG ACG GAG	576
Glu Gly Val Asp Met Leu Asn Val Asn Val Pro Ser Asp Ala Thr Glu	
180 185 190	
GAA ACG GAG ATA GCA ATC ACC CGC TTA GCC CGG AAG CGC TAC TCC CCA	624
Glu Thr Glu Ile Ala Ile Thr Arg Leu Ala Arg Lys Arg Tyr Ser Pro	
195 200 205	
ACG GTC GAG GAG AGG ATT GAC CCC AAG GGC AAC CCC TAC TAC TGG ATT	672
Thr Val Glu Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr Trp Ile	
210 215 220	
GTC GGC AAA CTT GTC CAA GAC TTC GAG CCA GGG ACA GAT GCC TAC GCC	720
Val Gly Lys Leu Val Gln Asp Phe Glu Pro Gly Thr Asp Ala Tyr Ala	
225 230 235 240	
CTG AAG GTC GAG AGG AAG GTC AGC GTC ACG CCG ATA AAC ATA GAT ATG	768
Leu Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile Asp Met	
245 250 255	
ACT GCG AGG GTG GAC TTT GAG GAG CTT GTA AGG GTT CTG TGG GTG	813
Thr Ala Arg Val Asp Phe Glu Glu Leu Val Arg Val Leu Trp Val	
260 265 270	
TAA	816

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG AAA GGA AAG TCT CTT GTT AGC GGT CTG TTG TTG GGT CTT TTA ATT	48
Met Lys Gly Lys Ser Leu Val Ser Gly Leu Leu Leu Gly Leu Leu Ile	
1 5 10 15	
TTG AGC CTG ATT TCA TTC CAG CCA AGC TTT GCA TAC TCC CCA CAC GGC	96
Leu Ser Leu Ile Ser Phe Gln Pro Ser Phe Ala Tyr Ser Pro His Gly	
20 25 30	
GGT GTC AAA AAC ATC ATA ATC CTG GTT GGA GAC GGC ATG GGT CTT GGG	144
Gly Val Lys Asn Ile Ile Ile Leu Val Gly Asp Gly Met Gly Leu Gly	
35 40 45	
CAT GTA GAA ATT ACA AAG CTC GTT TAT GGA CAC TTA AAC ATG GAA AAC	192
His Val Glu Ile Thr Lys Leu Val Tyr Gly His Leu Asn Met Glu Asn	
50 55 60	
TTT CCA GTT ACT GGA TTT GAG CTT ACT GAT TCC CTA AGT GGT GAA GTT	240
Phe Pro Val Thr Gly Phe Glu Leu Thr Asp Ser Leu Ser Gly Glu Val	
65 70 75 80	
ACA GAT TCT GCT GCG GCA GGA ACT GCA ATA TCC ACT GGA GCT AAA ACG	288
Thr Asp Ser Ala Ala Ala Gly Thr Ala Ile Ser Thr Gly Ala Lys Thr	
85 90 95	
TAT AAT GGT ATG ATT TCA GTA ACC AAC ATA ACC GGA AAG ATA GTT AAC	336
Tyr Asn Gly Met Ile Ser Val Thr Asn Ile Thr Gly Lys Ile Val Asn	
100 105 110	
TTA ACA ACC CTA CTT GAA GTG GCT CAA GAG CTT GGG AAG TCA ACA GGG	384
Leu Thr Thr Leu Leu Glu Val Ala Gln Glu Leu Gly Lys Ser Thr Gly	
115 120 125	
CTG GTC ACC ACA ACA AGG ATT ACC CAT GCA ACT CCA GCA GTT TTT GCG	432
Leu Val Thr Thr Thr Arg Ile Thr His Ala Thr Pro Ala Val Phe Ala	
130 135 140	
TCC CAT GTC CCA GAT AGG GAT ATG GAG GGG GAG ATA CCC AAG CAA CTC	480
Ser His Val Pro Asp Arg Asp Met Glu Gly Glu Ile Pro Lys Gln Leu	
145 150 155 160	
ATA ATG CAC AAA GTT AAC GTC TTG TTG GGT GGT GGA AGG GAG AAA TTC	528
Ile Met His Lys Val Asn Val Leu Leu Gly Gly Gly Arg Glu Lys Phe	
165 170 175	
GAT GAG AAA AAT TTG GAG CTG GCC AAA AAG CAG GGA TAC AAA GTA GTT	576
Asp Glu Lys Asn Leu Glu Leu Ala Lys Lys Gln Gly Tyr Lys Val Val	
180 185 190	
TTC ACG AAG GAA GAG CTT GAA AAA GTT GAA GGA GAT TAT GTC CTA GGA	624
Phe Thr Lys Glu Glu Leu Glu Lys Val Glu Gly Asp Tyr Val Leu Gly	
195 200 205	
CTC TTT GCA GAA AGT CAC ATC CCT TAC GTA TTG GAT AGA AAA CCC GAT	672
Leu Phe Ala Glu Ser His Ile Pro Tyr Val Leu Asp Arg Lys Pro Asp	
210 215 220	
GAT GTT GGA CTT TTA GAA ATG GCC AAA AAG GCA ATT TCA ATA CTC GAG	720
Asp Val Gly Leu Leu Glu Met Ala Lys Lys Ala Ile Ser Ile Leu Glu	
225 230 235 240	
AAG AAC CCG AGC GGA TTC TTT CTC ATG GTT GAG GGC GGA AGG ATT GAC	768
Lys Asn Pro Ser Gly Phe Phe Leu Met Val Glu Gly Gly Arg Ile Asp	

245										250					255					
CAT	GCA	GCC	CAT	GGA	AAC	GAT	GTC	GCA	TCG	GTT	GTT	GCA	GAA	ACT	AAG	816				
His	Ala	Ala	His	Gly	Asn	Asp	Val	Ala	Ser	Val	Val	Ala	Glu	Thr	Lys					
260				265				270												
GAG	TTT	GAC	GAT	GTT	GTC	AGA	TAC	GTG	CTG	GAA	TAT	CCG	AAG	AAG	AGG	864				
Glu	Phe	Asp	Asp	Val	Val	Arg	Tyr	Val	Leu	Glu	Tyr	Pro	Lys	Lys	Arg					
275				280				285												
GGA	GAT	ACC	TTG	GTA	ATA	GTG	CTT	GCC	GAT	CAC	GAA	ACT	GGA	GGT	CTT	912				
Gly	Asp	Thr	Leu	Val	Ile	Val	Leu	Ala	Asp	His	Glu	Thr	Gly	Gly	Leu					
290				295				300												
GCA	ATA	GGT	CTA	ACG	TAT	GGA	AAT	GCA	ATC	GAT	GAA	GAT	GCC	ATA	AGA	960				
Ala	Ile	Gly	Leu	Thr	Tyr	Gly	Asn	Ala	Ile	Asp	Glu	Asp	Ala	Ile	Arg					
305				310				315				320								
AAA	ATA	AAA	GCA	AGC	ACG	TTG	AGG	ATG	CCC	AAA	GAG	GTT	AAG	GCA	GGG	1008				
Lys	Ile	Lys	Ala	Ser	Thr	Leu	Arg	Met	Pro	Lys	Glu	Val	Lys	Ala	Gly					
325				330				335												
AGT	AGT	GTA	AAA	GAG	TCC	TCA	AAG	GTA	TGC	CGG	ATT	TGT	CCC	AAC	AGA	1056				
Ser	Ser	Val	Lys	Glu	Ser	Ser	Lys	Val	Cys	Arg	Ile	Cys	Pro	Asn	Arg					
340				345				350												
GGA	AGA	AGT	CAG	TAT	ATT	GAG	AAT	GCG	CTG	CAC	TCG	ACA	AAC	AAG	TAT	1104				
Gly	Arg	Ser	Gln	Tyr	Ile	Glu	Asn	Ala	Leu	His	Ser	Thr	Asn	Lys	Tyr					
355				360				365												
GCC	CTC	TCA	AAT	GCA	GTA	GCC	GAT	GTT	ATA	AAC	AGG	CGT	ATT	GGT	GTT	1152				
Ala	Leu	Ser	Asn	Ala	Val	Ala	Asp	Val	Ile	Asn	Arg	Arg	Ile	Gly	Val					
370				375				380												
GGA	TTC	ACC	TCC	TAT	GAG	CAT	ACA	GGA	GTT	CCA	GTT	CCG	CTC	TTA	GCT	1200				
Gly	Phe	Thr	Ser	Tyr	Glu	His	Thr	Gly	Val	Pro	Val	Pro	Leu	Leu	Ala					
385				390				395				400								
TAC	GGT	CCC	GGG	GCA	GAG	AAC	TTC	AGA	GGT	TTC	TTA	CAC	CAT	GTG	GAT	1248				
Tyr	Gly	Pro	Gly	Ala	Glu	Asn	Phe	Arg	Gly	Phe	Leu	His	His	Val	Asp					
405				410				415												
ACA	GCA	AGA	TTA	GTT	GCA	AAG	TTA	ATG	CTC	TTT	GGA	AGG	AGG	AAT	ATT	1296				
Thr	Ala	Arg	Leu	Val	Ala	Lys	Leu	Met	Leu	Phe	Gly	Arg	Arg	Asn	Ile					
420				425				430												
CCA	GTT	ACC	ATT	TCA	AGC	GTG	AGC	AGT	GTT	AAG	GGA	GAC	ATA	ACC	GGT	1344				
Pro	Val	Thr	Ile	Ser	Ser	Val	Ser	Ser	Val	Lys	Gly	Asp	Ile	Thr	Gly					
435				440				445												
GAT	TAC	AGG	GTT	GAT	GAG	AAG	GAT	GCC	TAC	GTT	ACG	CTC	ATG	ATG	TTT	1392				
Asp	Tyr	Arg	Val	Asp	Glu	Lys	Asp	Ala	Tyr	Val	Thr	Leu	Met	Met	Phe					
450				455				460												
CTC	GGA	GAA	AAA	GTG	GAT	AAT	GAA	ATT	GAA	AAG	AGA	GTC	GAT	ATA	GAC	1440				
Leu	Gly	Glu	Lys	Val	Asp	Asn	Glu	Ile	Glu	Lys	Arg	Val	Asp	Ile	Asp					
465				470				475				480								
AAC	AAC	GGC	ATG	GTT	GAC	TTA	AAT	GAC	GTC	ATG	TTG	ATT	CTC	CAG	GAA	1488				
Asn	Asn	Gly	Met	Val	Asp	Leu	Asn	Asp	Val	Met	Leu	Ile	Leu	Gln	Glu					
485				490				495												
GCT	TGA														1494					
Ala																				

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG CCA AGA AAT ATC GCC GCT GTA TGC GCC CTG GCC GCT TTG TTA GGG	48
Met Pro Arg Asn Ile Ala Ala Val Cys Ala Leu Ala Ala Leu Leu Gly	
1 5 10 15	
TCG GCC TGG GCG GCC AAA GTT GCC GTC TAC CCC TAC GAC GGA GCC GCT	96
Ser Ala Trp Ala Ala Lys Val Ala Val Tyr Pro Tyr Asp Gly Ala Ala	
20 25 30	
TTG CTG GCG GGG CAG CGC TTC GAT TTG CGC ATA GAA GCC TCC GAG CTG	144
Leu Leu Ala Gly Gln Arg Phe Asp Leu Arg Ile Glu Ala Ser Glu Leu	
35 40 45	
AAA GGC AAT TTA AAG GCT TAC CGC ATC ACC CTG GAC GGC CAG CCT CTG	192
Lys Gly Asn Leu Lys Ala Tyr Arg Ile Thr Leu Asp Gly Gln Pro Leu	
50 55 60	
GCG GGC CTC GAG CAA ACC GCG CAG GGG GCC GGG CAG GCC GAG TGG ACC	240
Ala Gly Leu Glu Gln Thr Ala Gln Gly Ala Gly Gln Ala Glu Trp Thr	
65 70 75 80	
CTG CGC GGT GCC TTC CTG CGC CCT GGA AGC CAC ACC CTC GAG GTC AGC	288
Leu Arg Gly Ala Phe Leu Arg Pro Gly Ser His Thr Leu Glu Val Ser	
85 90 95	
CTC ACC GAC GAC GCT GGG GAG AGC AGG AAG AGC GTA CGT TGG GAG GCT	336
Leu Thr Asp Asp Ala Gly Glu Ser Arg Lys Ser Val Arg Trp Glu Ala	
100 105 110	
CGG CAG AAC CTT CGC TTG CCC CGA GCG GCC AAG AAT GTG ATT CTC TTC	384
Arg Gln Asn Leu Arg Leu Pro Arg Ala Ala Lys Asn Val Ile Leu Phe	
115 120 125	
ATT GGC GAC GGG ATG GGC TGG AAC ACC CTC AAC GCC GCC CGC ATC ATC	432
Ile Gly Asp Gly Met Gly Trp Asn Thr Leu Asn Ala Ala Arg Ile Ile	
130 135 140	
GCC AAA GGC TTT AAC CCC GAA AAC GGT ATG CCC AAC GGA AAC CTC GAG	480
Ala Lys Gly Phe Asn Pro Glu Asn Gly Met Pro Asn Gly Asn Leu Glu	
145 150 155 160	
ATC GAG AGT GGT TAC GGT GGG ATG GCT ACC GTC ACT ACC GGC AGC TTT	528
Ile Glu Ser Gly Tyr Gly Gly Met Ala Thr Val Thr Thr Gly Ser Phe	
165 170 175	
GAT AGC TTC ATC GCC GAC TCA GCT AAC TCG GCT TCT TCC ATC ATG ACC	576
Asp Ser Phe Ile Ala Asp Ser Ala Asn Ser Ala Ser Ser Ile Met Thr	
180 185 190	

GGG CAG AAG GTG CAG GTG AAT GCC CTC AAC GTT TAC CCA TCA AAC CTC Gly Gln Lys Val Gln Val Asn Ala Leu Asn Val Tyr Pro Ser Asn Leu 195 200 205	624
AAA GAT ACC CTG GCC TAC CCC CGG ATC GAA ACC CTA GCG GAG ATG CTC Lys Asp Thr Leu Ala Tyr Pro Arg Ile Glu Thr Leu Ala Glu Met Leu 210 215 220	672
AAG CGG GTA CGC GGG GCC AGC ATT GGG GTA GTG ACC ACC ACC TTC GGC Lys Arg Val Arg Gly Ala Ser Ile Gly Val Val Thr Thr Thr Phe Gly 225 230 235 240	720
ACC GAC GCT ACC CCG GCT TCA CTC AAC GCC CAT ACC CGC CGC CGC GGT Thr Asp Ala Thr Pro Ala Ser Leu Asn Ala His Thr Arg Arg Arg Gly 245 250 255	768
GAT TAC CAG GCT ATC GCC GAC ATG TAC TTT GGT AGA GGC GGG TTC GGT Asp Tyr Gln Ala Ile Ala Asp Met Tyr Phe Gly Arg Gly Gly Phe Gly 260 265 270	816
GTT CCC TTG GAT GTG ATG CTC TTC GGT GGT TCA CGC GAC TTC ATC CCC Val Pro Leu Asp Val Met Leu Phe Gly Gly Ser Arg Asp Phe Ile Pro 275 280 285	864
CAG AGC ACC CCT GGC TCG CGG CGC AAG GAT AGC ACG GAC TGG ATT GCC Gln Ser Thr Pro Gly Ser Arg Arg Lys Asp Ser Thr Asp Trp Ile Ala 290 295 300	912
GAA TCC CAG AAG CTG GGC TAC ACC TTT GTC AGC ACC CGC AGC GAG CTG Glu Ser Gln Lys Leu Gly Tyr Thr Phe Val Ser Thr Arg Ser Glu Leu 305 310 315 320	960
CTG GCG GCC AAA CCC ACC GAT AAG CTG TTT GGG CTG TTC AAC ATT GAC Leu Ala Ala Lys Pro Thr Asp Lys Leu Phe Gly Leu Phe Asn Ile Asp 325 330 335	1008
AAC TTC CCC AGC TAC CTA GAC CGC GCA GTG TGG AAG CGG CCC GAG ATG Asn Phe Pro Ser Tyr Leu Asp Arg Ala Val Trp Lys Arg Pro Glu Met 340 345 350	1056
CTG GGA AGC TTT ACC GAT ATG CCC TAC CTC TGG GAG ATG ACC CAG AAA Leu Gly Ser Phe Thr Asp Met Pro Tyr Leu Trp Glu Met Thr Gln Lys 355 360 365	1104
GCC GTG GAG GCT CTC TCC AGA AAC GAC AAA GGC TTT TTC TTG ATG GTT Ala Val Glu Ala Leu Ser Arg Asn Asp Lys Gly Phe Phe Leu Met Val 370 375 380	1152
GAG GGG GGA ATG GTG GAT AAG TAC GAG CAC CCC TTG GAC TGG CCC CGC Glu Gly Gly Met Val Asp Lys Tyr Glu His Pro Leu Asp Trp Pro Arg 385 390 395 400	1200
GCA CTT TGG GAT GTA CTC GAG CTG GAC CGC GCG GTG GCT TGG GCC AAG Ala Leu Trp Asp Val Leu Glu Leu Asp Arg Ala Val Ala Trp Ala Lys 405 410 415	1248
GGC TAT GCG GCC TCC CAC CCC GAT ACC CTG GTG ATT GTC ACC GCC GAC Gly Tyr Ala Ala Ser His Pro Asp Thr Leu Val Ile Val Thr Ala Asp 420 425 430	1296
CAC GCT CAC TCG ATC TCG GTG TTT GGC GGT TAC GAC TAC TCC AAG CAG His Ala His Ser Ile Ser Val Phe Gly Gly Tyr Asp Tyr Ser Lys Gln 435 440 445	1344
GGC CGG GAG GGG GTG GGG GTT TAT GAG GCC GCC AAG TTC CCC ACC TAC	1392

Gly	Arg	Glu	Gly	Val	Gly	Val	Tyr	Glu	Ala	Ala	Lys	Phe	Pro	Thr	Tyr	
450					455						460					
GGC	GAC	AAA	AAA	GAC	GCC	AAC	GGC	TTT	CCC	TTG	CCC	GAC	ACC	ACT	CGG	1440
Gly	Asp	Lys	Lys	Asp	Ala	Asn	Gly	Phe	Pro	Leu	Pro	Asp	Thr	Thr	Arg	
465					470				475						480	
GGA	ATC	GCG	GTA	GGC	TTC	GGG	GCC	ACG	CCG	GAT	TAC	TGT	GAA	ACC	TAC	1488
Gly	Ile	Ala	Val	Gly	Phe	Gly	Ala	Thr	Pro	Asp	Tyr	Cys	Glu	Thr	Tyr	
			485					490						495		
CGG	GGC	CGC	GAG	GTC	TAC	AAA	GAC	CCC	ACC	ATC	TCC	GAC	GGC	AAA	GGT	1536
Arg	Gly	Arg	Glu	Val	Tyr	Lys	Asp	Pro	Thr	Ile	Ser	Asp	Gly	Lys	Gly	
			500					505					510			
GGT	TAC	GTG	GCC	AAC	CCT	GAG	GTC	TGC	AAG	GAG	CCG	GGC	CTT	CCA	ACG	1584
Gly	Tyr	Val	Ala	Asn	Pro	Glu	Val	Cys	Lys	Glu	Pro	Gly	Leu	Pro	Thr	
	515					520						525				
TAC	CGG	CAA	CTC	CCA	GTA	GAT	AGC	GCC	CAG	GGC	GTG	CAC	ACG	GCT	GAT	1632
Tyr	Arg	Gln	Leu	Pro	Val	Asp	Ser	Ala	Gln	Gly	Val	His	Thr	Ala	Asp	
	530					535					540					
CCC	ATG	CCG	CTG	TTT	GCC	TTT	GGC	GTG	GGG	TCT	CAG	TTC	TTC	AAT	GGC	1680
Pro	Met	Pro	Leu	Phe	Ala	Phe	Gly	Val	Gly	Ser	Gln	Phe	Phe	Asn	Gly	
545					550					555					560	
CTC	ATC	GAC	CAG	ACC	GAG	ATC	TTC	TTC	CGC	ATG	GCC	CAG	GCC	CTA	GGG	1728
Leu	Ile	Asp	Gln	Thr	Glu	Ile	Phe	Phe	Arg	Met	Ala	Gln	Ala	Leu	Gly	
			565					570						575		
TTC	AAC	CCC	CAC	CTC	GAG	AAG	CCT	TAA								1755
Phe	Asn	Pro	His	Leu	Glu	Lys	Pro									
			580													

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG	TAT	AAA	TGG	ATT	ATT	GAG	GGT	AAG	CTT	GCC	CAA	GCA	CCT	TTT	CCA	48
Met	Tyr	Lys	Trp	Ile	Ile	Glu	Gly	Lys	Leu	Ala	Gln	Ala	Pro	Phe	Pro	
1				5					10					15		
AGC	CTA	GGT	GAA	CTA	GCC	GAT	CTC	AAA	AGA	CTT	TTC	GAC	GCC	ATT	ATT	96
Ser	Leu	Gly	Glu	Leu	Ala	Asp	Leu	Lys	Arg	Leu	Phe	Asp	Ala	Ile	Ile	
			20					25					30			
GTT	CTT	ACA	ATG	CCG	CAT	GAA	CAA	CCG	CTT	AAT	GAG	AAA	TAT	ATC	GAG	144
Val	Leu	Thr	Met	Pro	His	Glu	Gln	Pro	Leu	Asn	Glu	Lys	Tyr	Ile	Glu	
			35					40				45				
ATA	TTA	GAG	AGC	CAT	GGA	TTC	CAA	GTC	CTC	CAT	GTC	CCC	ACG	CTC	GAC	192
Ile	Leu	Glu	Ser	His	Gly	Phe	Gln	Val	Leu	His	Val	Pro	Thr	Leu	Asp	

50	55	60	
TTT CAT CCT TTA GAA CTC TTC GAC CTT TTG AAA ACA AGC ATA TTC ATT	240		
Phe His Pro Leu Glu Leu Phe Asp Leu Leu Lys Thr Ser Ile Phe Ile			
65 70 75 80			
GAT GAA AAC CTG GAG AGA TCC CAC AGA GTG CTT GTC CAC TGC ATG GGA	288		
Asp Glu Asn Leu Glu Arg Ser His Arg Val Leu Val His Cys Met Gly			
85 90 95			
GGC ATA GGC CGG AGC GGG CTT GTA ACT GCT GCG TAC TTA ATA TTC AAA	336		
Gly Ile Gly Arg Ser Gly Leu Val Thr Ala Ala Tyr Leu Ile Phe Lys			
100 105 110			
GGT TAT GAT ATT TAC GAC GCG GTA AAG CAT GTG AGA ACG GTA GTG CCT	384		
Gly Tyr Asp Ile Tyr Asp Ala Val Lys His Val Arg Thr Val Val Pro			
115 120 125			
GGT GCT ATT GAA AAC AGA GGG CAA GCG TTA ATG CTT GAG AAC TAC TAT	432		
Gly Ala Ile Glu Asn Arg Gly Gln Ala Leu Met Leu Glu Asn Tyr Tyr			
130 135 140			
ACC CTG GTC AAA AGT TTC AAC AGA GAG TTG CTG AGA GAC TAC GGG AAG	480		
Thr Leu Val Lys Ser Phe Asn Arg Glu Leu Arg Asp Tyr Gly Lys			
145 150 155 160			
AAA ATT TTC ACG CTC GGT GAC CCG AAG GCG GTT CTC CAC GCT TCT AAG	528		
Lys Ile Phe Thr Leu Gly Asp Pro Lys Ala Val Leu His Ala Ser Lys			
165 170 175			
ACG ACT CAG TTC ACG ATT GAA CTC TTA AGC AAC TTA CAC GTC AAC GAG	576		
Thr Thr Gln Phe Thr Ile Glu Leu Leu Ser Asn Leu His Val Asn Glu			
180 185 190			
GCG TTT TCA ATC AGT GCG ATG GCT CAA TCA CTG CTC CAC TTT CAC GAC	624		
Ala Phe Ser Ile Ser Ala Met Ala Gln Ser Leu Leu His Phe His Asp			
195 200 205			
GTA AAA GTC CGC TCT AAA CTG AAA GAA GTA TTC GAA AAC ATG GAA TTC	672		
Val Lys Val Arg Ser Lys Leu Lys Glu Val Phe Glu Asn Met Glu Phe			
210 215 220			
TCA TCC GCC TCA GAG GAG GTT CTG TCA TTT ATT CAC CTA CTC GAT TTC	720		
Ser Ser Ala Ser Glu Glu Val Leu Ser Phe Ile His Leu Leu Asp Phe			
225 230 235 240			
TAT CAG GAT GGC AGG GTT GTT TTA ACC ATT TAC GAT TAT CTC CCC GAT	768		
Tyr Gln Asp Gly Arg Val Val Leu Thr Ile Tyr Asp Tyr Leu Pro Asp			
245 250 255			
AGG GTG GAT TTG ATT TTA TTG TGT AAG TGG GGT TGT GAT AAA ATA GTT	816		
Arg Val Asp Leu Ile Leu Leu Cys Lys Trp Gly Cys Asp Lys Ile Val			
260 265 270			
GAA GTC TCG TCT TCA GCG AAG AAA ACC GTT GAG AAG CTT GTA GGA AGA	864		
Glu Val Ser Ser Ser Ala Lys Lys Thr Val Glu Lys Leu Val Gly Arg			
275 280 285			
AAG GTT TCC CTA TCC TGG GCT AAT TAC TTA GAC TAT GTT TAG	906		
Lys Val Ser Leu Ser Trp Ala Asn Tyr Leu Asp Tyr Val			
290 295 300			

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG AGA ATC CTC CTC ACC AAC GAC GAC GGC ATC TAT TCC AAC GGT CTG	48
Met Arg Ile Leu Leu Thr Asn Asp Asp Gly Ile Tyr Ser Asn Gly Leu	
1 5 10 15	
CGC GCG GCG GTG AAG GGC CTG AGC GAG CTC GGC GAG GTC TAC GTC GTC	96
Arg Ala Ala Val Lys Gly Leu Ser Glu Leu Gly Glu Val Tyr Val Val	
20 25 30	
GCC CCG CTC TTC CAG AGG AGC GCG AGC GGT CCG GCG ATG ACC CTA CAC	144
Ala Pro Leu Phe Gln Arg Ser Ala Ser Gly Arg Ala Met Thr Leu His	
35 40 45	
AGG CCG ATA AGG GCA AAG AGG GTT GAC GTT CCC GGC GCG AAG ATA GCG	192
Arg Pro Ile Arg Ala Lys Arg Val Asp Val Pro Gly Ala Lys Ile Ala	
50 55 60	
TAT GGC ATA GAC GGA ACG CCG ACC GAC TGC GTG ATT TTT GCC ATC GCC	240
Tyr Gly Ile Asp Gly Thr Pro Thr Asp Cys Val Ile Phe Ala Ile Ala	
65 70 75 80	
CGC TTC GGC GAC TTT GAT CTG GCG GTC AGC GGG ATA AAC CTA GGC GAG	288
Arg Phe Gly Asp Phe Asp Leu Ala Val Ser Gly Ile Asn Leu Gly Glu	
85 90 95	
AAC CTG AGC ACG GAG ATA ACC GTC TCC GGA ACG GCC TCG GCG GCG ATA	336
Asn Leu Ser Thr Glu Ile Thr Val Ser Gly Thr Ala Ser Ala Ala Ile	
100 105 110	
GAG GCT TCC ACC CAC GGG ATT CCA AGT GTA GCT ATA AGC CTC GAG GTC	384
Glu Ala Ser Thr His Gly Ile Pro Ser Val Ala Ile Ser Leu Glu Val	
115 120 125	
GAG TGG AAG AAG ACC CTC GGC GAG GGG GAG GGT ATT GAC TTC TCG GTT	432
Glu Trp Lys Lys Thr Leu Gly Glu Gly Glu Gly Ile Asp Phe Ser Val	
130 135 140	
TCA GCA CAC TTC CTG AGA AGG ATA GCG ACG GCT GTC CTT AAG AAG GGC	480
Ser Ala His Phe Leu Arg Arg Ile Ala Thr Ala Val Leu Lys Lys Gly	
145 150 155 160	
CTG CCT GAA GGG GTG GAC ATG CTC AAC GTG AAC GTC CCT AGC GAC GCC	528
Leu Pro Glu Gly Val Asp Met Leu Asn Val Asn Val Pro Ser Asp Ala	
165 170 175	
AGC GAG GGG ACT GAG ATC GCC ATA ACG CGC CTC GCG AGG AAG CGC TAT	576
Ser Glu Gly Thr Glu Ile Ala Ile Thr Arg Leu Ala Arg Lys Arg Tyr	
180 185 190	
TCT CCG ACG ATA GAG GAG AGG ATA GAC CCC AAG GGC AAC CCC TAC TAC	624
Ser Pro Thr Ile Glu Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr	
195 200 205	

TGG ATC GTT GGC AGG CTC GTC CAG GAG TTC GAG CCG GGC ACG GAC GCC	672
Trp Ile Val Gly Arg Leu Val Gln Glu Phe Glu Pro Gly Thr Asp Ala	
210 215 220	
TAC GCT CTG AAA GTC GAG AGA AAG GTC AGC GTC ACG CCC ATA AAC ATC	720
Tyr Ala Leu Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile	
225 230 235 240	
GAC ATG ACT GCG AGG GTT GAC TTT GAG AAC CTT CAA AGG CTT CTG AGC	768
Asp Met Thr Ala Arg Val Asp Phe Glu Asn Leu Gln Arg Leu Leu Ser	
245 250 255	
CTG TGA	774
Leu	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAA AAC TTA AAA AAG TAC CTA GAA GTT GCA AAA ATA GCC GCG CTC	48
Met Glu Asn Leu Lys Lys Tyr Leu Glu Val Ala Lys Ile Ala Ala Leu	
1 5 10 15	
GCG GGT GGG CAG GTT CTG AAA GAA AAC TTC GGA AAG GTA AAA AAG GAA	96
Ala Gly Gly Gln Val Leu Lys Glu Asn Phe Gly Lys Val Lys Lys Glu	
20 25 30	
AAC ATA GAG GAA AAA GGG GAA AAG GAC TTT GTA AGT TAC GTG GAT AAA	144
Asn Ile Glu Glu Lys Gly Glu Lys Asp Phe Val Ser Tyr Val Asp Lys	
35 40 45	
ACT TCA GAG GAA AGG ATA AAG GAG GTG ATA CTC AAG TTC TTT CCC GAT	192
Thr Ser Glu Glu Arg Ile Lys Glu Val Ile Leu Lys Phe Phe Pro Asp	
50 55 60	
CAC GAG GTC GTA GGG GAA GAG ATG GGT GCG GAG GGA AGC GGA AGC GAA	240
His Glu Val Val Gly Glu Glu Met Gly Ala Glu Gly Ser Gly Ser Glu	
65 70 75 80	
TAC AGG TGG TTC ATA GAC CCC CTT GAC GGC ACA AAG AAC TAC ATA AAC	288
Tyr Arg Trp Phe Ile Asp Pro Leu Asp Gly Thr Lys Asn Tyr Ile Asn	
85 90 95	
GGT TTT CCC ATC TTT GCC GTA TCA GTG GGA CTT GTT AAG GGA GAA GAG	336
Gly Phe Pro Ile Phe Ala Val Ser Val Gly Leu Val Lys Gly Glu Glu	
100 105 110	
CCA ATT GTG GGT GCG GTT TAC CTT CCT TAC TTT GAC AAG CTT TAC TGG	384
Pro Ile Val Gly Ala Val Tyr Leu Pro Tyr Phe Asp Lys Leu Tyr Trp	
115 120 125	
GGT GCT AAA GGT CTC GGG GCT TAC GTA AAC GGA AAG AGG ATA AAG GTA	432

Gly	Ala	Lys	Gly	Leu	Gly	Ala	Tyr	Val	Asn	Gly	Lys	Arg	Ile	Lys	Val	
130						135					140					
AAG	GAC	AAT	GAG	AGT	TTA	AAG	CAC	GCC	GGA	GTG	GTT	TAC	GGA	TTT	CCC	480
Lys	Asp	Asn	Glu	Ser	Leu	Lys	His	Ala	Gly	Val	Val	Tyr	Gly	Phe	Pro	
145					150				155					160		
TCT	AGG	AGC	AGG	AGG	GAC	ATA	TCT	ATC	TAC	TTG	AAC	ATA	TTC	AAG	GAT	528
Ser	Arg	Ser	Arg	Arg	Asp	Ile	Ser	Ile	Tyr	Leu	Asn	Ile	Phe	Lys	Asp	
				165					170					175		
GTC	TTT	TAC	GAA	GTT	GGC	TCT	ATG	AGG	AGA	CCC	GGG	GCT	GCT	GCG	GTT	576
Val	Phe	Tyr	Glu	Val	Gly	Ser	Met	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Val	
			180					185					190			
GAC	CTC	TGC	ATG	GTG	GCG	GAA	GGG	ATA	TTT	GAC	GGG	ATG	ATG	GAG	TTT	624
Asp	Leu	Cys	Met	Val	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe	
		195				200					205					
GAA	ATG	AAG	CCG	TGG	GAC	ATA	ACC	GCA	GGG	CTT	GTA	ATA	CTG	AAG	GAA	672
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu	
	210					215					220					
GCC	GGG	GGC	GTT	TAC	ACA	CTT	GTG	GGA	GAA	CCC	TTC	GGA	GTT	TCG	GAC	720
Ala	Gly	Gly	Val	Tyr	Thr	Leu	Val	Gly	Glu	Pro	Phe	Gly	Val	Ser	Asp	
225					230					235					240	
ATA	ATT	GCG	GGC	AAC	AAA	GCC	CTC	CAC	GAC	TTT	ATA	CTT	CAG	GTA	GCC	768
Ile	Ile	Ala	Gly	Asn	Lys	Ala	Leu	His	Asp	Phe	Ile	Leu	Gln	Val	Ala	
				245					250					255		
AAA	AAG	TAT	ATG	GAA	GTG	GCG	GTG	TGA								795
Lys	Lys	Tyr	Met	Glu	Val	Ala	Val									
			260													

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Arg	Gly	Ser	Gly	Val	Arg	Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile	
1				5				10						15		
Phe	Ala	Glu	Gly	Leu	Gly	Ala	Leu	Arg	Lys	Met	Leu	Glu	Pro	Val	Ala	
		20						25					30			
Thr	Leu	Tyr	Val	Val	Ala	Pro	Asp	Arg	Glu	Arg	Ser	Ala	Ala	Ser	His	
	35						40				45					
Ala	Ile	Thr	Val	His	Arg	Pro	Leu	Arg	Val	Arg	Glu	Ala	Gly	Phe	Arg	
	50					55				60						
Ser	Pro	Arg	Leu	Lys	Gly	Trp	Val	Val	Asp	Gly	Thr	Pro	Ala	Asp	Cys	
65				70					75					80		
Val	Lys	Leu	Gly	Leu	Glu	Val	Leu	Leu	Pro	Glu	Arg	Pro	Asp	Phe	Leu	
			85					90						95		
Val	Ser	Gly	Ile	Asn	Tyr	Gly	Pro	Asn	Leu	Gly	Thr	Asp	Val	Leu	Tyr	
		100					105						110			
Ser	Gly	Thr	Val	Ser	Ala	Ala	Ile	Glu	Gly	Val	Ile	Asn	Gly	Ile	Pro	
	115						120					125				
Ser	Val	Ala	Val	Ser	Leu	Ala	Thr	Arg	Arg	Glu	Pro	Asp	Tyr	Thr	Trp	

130	135	140
Ala Ala Arg Phe Val	Leu Val Leu Leu Glu Glu	Leu Arg Lys His Gln
145	150	155
Leu Pro Pro Gly Thr	Leu Leu Asn Val Asn Val	Pro Asp Gly Val Pro
	165	170
Arg Gly Val Lys Val	Thr Lys Leu Gly Ser Val	Arg Tyr Val Asn Val
	180	185
Val Asp Cys Arg Thr	Asp Pro Arg Gly Lys Ala Tyr	Tyr Trp Met Ala
	195	200
Gly Glu Pro Leu Glu	Leu Asp Gly Asn Asp Ser Glu	Thr Asp Val Trp
	210	215
Ala Val Arg Glu Gly	Tyr Ile Ser Val Thr Pro	Val Gln Ile Asp Leu
225	230	235
Thr Asn Tyr Gly Phe	Leu Glu Glu Leu Lys Lys	Trp Arg Phe Lys Asp
	245	250
Ile Phe Ser Ser		255
	260	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Leu	Asp	Ile	Leu	Leu	Val	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly
1				5					10					15	
Leu	Ile	Ala	Leu	Lys	Asp	Ala	Leu	Leu	Glu	Lys	Phe	Asn	Ala	Arg	Ile
		20						25					30		
Thr	Ile	Val	Ala	Pro	Thr	Asn	Gln	Gln	Ser	Gly	Ile	Gly	Arg	Ala	Ile
		35					40					45			
Ser	Leu	Phe	Glu	Pro	Leu	Arg	Ile	Thr	Lys	Thr	Lys	Leu	Ala	Asp	Gly
	50					55					60				
Ser	Trp	Gly	Tyr	Ala	Val	Ser	Gly	Thr	Pro	Thr	Asp	Cys	Val	Ile	Leu
	65				70				75					80	
Gly	Ile	Tyr	Glu	Ile	Leu	Lys	Lys	Val	Pro	Asp	Val	Val	Ile	Ser	Gly
			85					90						95	
Ile	Asn	Ile	Gly	Glu	Asn	Leu	Gly	Thr	Glu	Ile	Thr	Thr	Ser	Gly	Thr
		100					105						110		
Leu	Gly	Ala	Ala	Phe	Glu	Gly	Ala	His	His	Gly	Ala	Lys	Ala	Leu	Ala
		115					120					125			
Ser	Ser	Leu	Gln	Val	Thr	Ser	Asp	His	Leu	Lys	Phe	Lys	Glu	Gly	Glu
	130					135					140				
Thr	Pro	Ile	Asp	Phe	Thr	Val	Pro	Ala	Arg	Ile	Thr	Ala	Asn	Val	Val
	145				150					155				160	
Glu	Lys	Met	Leu	Asp	Tyr	Asp	Phe	Pro	Cys	Asp	Val	Val	Asn	Leu	Asn
			165						170					175	
Ile	Pro	Glu	Gly	Ala	Thr	Glu	Lys	Thr	Pro	Ile	Glu	Ile	Thr	Arg	Leu
		180					185						190		
Ala	Arg	Lys	Met	Tyr	Thr	Thr	His	Val	Glu	Glu	Arg	Ile	Asp	Pro	Arg
		195					200					205			
Gly	Arg	Ser	Tyr	Tyr	Trp	Ile	Asp	Gly	Tyr	Pro	Ile	Leu	Glu	Glu	Glu
	210					215					220				
Glu	Asp	Thr	Asp	Val	Tyr	Val	Val	Arg	Arg	Lys	Gly	His	Ile	Ser	Leu
	225				230					235				240	
Thr	Pro	Leu	Thr	Leu	Asp	Thr	Thr	Ile	Lys	Asn	Leu	Glu	Glu	Phe	Lys
			245						250					255	
Lys	Lys	Tyr	Glu	Arg	Ile	Leu	Asn	Glu							
			260					265							

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Met	Met	Glu	Phe	Thr	Arg	Glu	Gly	Ile	Lys	Ala	Ala	Val	Glu	Ala
1				5					10					15	
Leu	Gln	Gly	Leu	Gly	Glu	Ile	Tyr	Val	Val	Ala	Pro	Met	Phe	Gln	Arg
			20					25					30		
Ser	Ala	Ser	Gly	Arg	Ala	Met	Thr	Ile	His	Arg	Pro	Leu	Arg	Ala	Lys
		35					40					45			
Arg	Ile	Ser	Met	Asn	Gly	Ala	Lys	Ala	Ala	Tyr	Ala	Leu	Asp	Gly	Met
	50					55					60				
Pro	Val	Asp	Cys	Val	Ile	Phe	Ala	Met	Ala	Arg	Phe	Gly	Asp	Phe	Asp
65					70					75				80	
Leu	Ala	Ile	Ser	Gly	Val	Asn	Leu	Gly	Glu	Asn	Met	Ser	Thr	Glu	Ile
				85					90					95	
Thr	Val	Ser	Gly	Thr	Ala	Ser	Ala	Ala	Ile	Glu	Ala	Ala	Thr	Gln	Glu
			100					105					110		
Ile	Pro	Ser	Ile	Pro	Ile	Ser	Leu	Glu	Val	Asn	Arg	Glu	Lys	His	Lys
		115					120					125			
Phe	Gly	Glu	Gly	Glu	Glu	Ile	Asp	Phe	Ser	Ala	Ala	Lys	Tyr	Phe	Leu
	130					135				140					
Arg	Lys	Ile	Ala	Thr	Ala	Val	Leu	Lys	Arg	Gly	Leu	Pro	Lys	Gly	Val
145					150					155				160	
Asp	Met	Leu	Asn	Val	Asn	Val	Pro	Tyr	Asp	Ala	Asn	Glu	Arg	Thr	Glu
			165						170				175		
Ile	Ala	Phe	Thr	Arg	Leu	Ala	Arg	Arg	Met	Tyr	Arg	Pro	Ser	Ile	Glu
			180					185					190		
Glu	Arg	Ile	Asp	Pro	Lys	Gly	Asn	Pro	Tyr	Tyr	Trp	Ile	Val	Gly	Thr
		195					200					205			
Gln	Cys	Pro	Lys	Glu	Ala	Leu	Glu	Pro	Gly	Thr	Asp	Met	Tyr	Val	Val
	210					215					220				
Lys	Val	Glu	Arg	Lys	Val	Ser	Val	Thr	Pro	Ile	Asn	Ile	Asp	Met	Thr
225					230					235				240	
Ala	Arg	Val	Asn	Leu	Asp	Glu	Ile	Lys	Arg	Leu	Leu	Glu	Leu		
			245						250						

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Arg	Thr	Leu	Thr	Ile	Asn	Thr	Asp	Ala	Glu	Gly	Phe	Val	Leu	Arg
1				5					10					15	
Ile	Leu	Leu	Thr	Asn	Asp	Asp	Gly	Ile	Tyr	Ser	Asn	Gly	Leu	Arg	Ala
			20					25				30			
Ala	Val	Lys	Ala	Leu	Ser	Glu	Leu	Gly	Glu	Val	Tyr	Val	Val	Ala	Pro

Leu	Phe	35	Gln	Arg	Ser	Ala	Ser	40	Gly	Arg	Ala	Met	Thr	45	Leu	His	Arg	Pro
50							55						60					
Ile	Arg	Ala	Lys	Arg	Val	Asp	Val	Pro	Gly	Ala	Lys	Ile	Ala	Tyr	Gly			
65						70				75					80			
Ile	Asp	Gly	Thr	Pro	Thr	Asp	Cys	Val	Ile	Phe	Ala	Ile	Ala	Arg	Phe			
					85				90					95				
Gly	Ser	Phe	Gly	Leu	Ala	Val	Ser	Gly	Ile	Asn	Leu	Gly	Glu	Asn	Leu			
			100					105					110					
Ser	Thr	Glu	Ile	Thr	Val	Ser	Gly	Thr	Ala	Ser	Ala	Ala	Ile	Glu	Ala			
		115						120					125					
Ser	Thr	His	Gly	Ile	Pro	Ser	Ile	Ala	Ile	Ser	Leu	Glu	Val	Glu	Trp			
130						135					140							
Lys	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Gly	Val	Asp	Phe	Ser	Val	Ser	Thr			
145					150					155					160			
His	Phe	Leu	Lys	Arg	Ile	Ala	Gly	Ala	Leu	Leu	Glu	Arg	Gly	Leu	Pro			
			165						170					175				
Glu	Gly	Val	Asp	Met	Leu	Asn	Val	Asn	Val	Pro	Ser	Asp	Ala	Thr	Glu			
			180					185					190					
Glu	Thr	Glu	Ile	Ala	Ile	Thr	Arg	Leu	Ala	Arg	Lys	Arg	Tyr	Ser	Pro			
		195						200					205					
Thr	Val	Glu	Glu	Arg	Ile	Asp	Pro	Lys	Gly	Asn	Pro	Tyr	Tyr	Trp	Ile			
210					215						220							
Val	Gly	Lys	Leu	Val	Gln	Asp	Phe	Glu	Pro	Gly	Thr	Asp	Ala	Tyr	Ala			
225					230					235					240			
Leu	Lys	Val	Glu	Arg	Lys	Val	Ser	Val	Thr	Pro	Ile	Asn	Ile	Asp	Met			
			245						250					255				
Thr	Ala	Arg	Val	Asp	Phe	Glu	Glu	Leu	Val	Arg	Val	Leu	Trp	Val				
			260					265					270					

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Lys	Gly	Lys	Ser	Leu	Val	Ser	Gly	Leu	Leu	Leu	Gly	Leu	Leu	Ile			
1				5					10					15				
Leu	Ser	Leu	Ile	Ser	Phe	Gln	Pro	Ser	Phe	Ala	Tyr	Ser	Pro	His	Gly			
		20						25					30					
Gly	Val	Lys	Asn	Ile	Ile	Ile	Leu	Val	Gly	Asp	Gly	Met	Gly	Leu	Gly			
		35					40					45						
His	Val	Glu	Ile	Thr	Lys	Leu	Val	Tyr	Gly	His	Leu	Asn	Met	Glu	Asn			
50					55					60								
Phe	Pro	Val	Thr	Gly	Phe	Glu	Leu	Thr	Asp	Ser	Leu	Ser	Gly	Glu	Val			
65				70					75					80				
Thr	Asp	Ser	Ala	Ala	Ala	Gly	Thr	Ala	Ile	Ser	Thr	Gly	Ala	Lys	Thr			
			85					90					95					
Tyr	Asn	Gly	Met	Ile	Ser	Val	Thr	Asn	Ile	Thr	Gly	Lys	Ile	Val	Asn			
		100					105					110						
Leu	Thr	Thr	Leu	Leu	Glu	Val	Ala	Gln	Glu	Leu	Gly	Lys	Ser	Thr	Gly			
		115					120					125						
Leu	Val	Thr	Thr	Thr	Arg	Ile	Thr	His	Ala	Thr	Pro	Ala	Val	Phe	Ala			
130					135						140							
Ser	His	Val	Pro	Asp	Arg	Asp	Met	Glu	Gly	Glu	Ile	Pro	Lys	Gln	Leu			
145				150					155					160				
Ile	Met	His	Lys	Val	Asn	Val	Leu	Leu	Gly	Gly	Gly	Arg	Glu	Lys	Phe			
			165						170					175				

Asp Glu Lys Asn Leu Glu Leu Ala Lys Lys Gln Gly Tyr Lys Val Val
 180 185 190
 Phe Thr Lys Glu Glu Leu Glu Lys Val Glu Gly Asp Tyr Val Leu Gly
 195 200 205
 Leu Phe Ala Glu Ser His Ile Pro Tyr Val Leu Asp Arg Lys Pro Asp
 210 215 220
 Asp Val Gly Leu Leu Glu Met Ala Lys Lys Ala Ile Ser Ile Leu Glu
 225 230 235 240
 Lys Asn Pro Ser Gly Phe Phe Leu Met Val Glu Gly Gly Arg Ile Asp
 245 250 255
 His Ala Ala His Gly Asn Asp Val Ala Ser Val Val Ala Glu Thr Lys
 260 265 270
 Glu Phe Asp Asp Val Val Arg Tyr Val Leu Glu Tyr Pro Lys Lys Arg
 275 280 285
 Gly Asp Thr Leu Val Ile Val Leu Ala Asp His Glu Thr Gly Gly Leu
 290 295 300
 Ala Ile Gly Leu Thr Tyr Gly Asn Ala Ile Asp Glu Asp Ala Ile Arg
 305 310 315 320
 Lys Ile Lys Ala Ser Thr Leu Arg Met Pro Lys Glu Val Lys Ala Gly
 325 330 335
 Ser Ser Val Lys Glu Ser Ser Lys Val Cys Arg Ile Cys Pro Asn Arg
 340 345 350
 Gly Arg Ser Gln Tyr Ile Glu Asn Ala Leu His Ser Thr Asn Lys Tyr
 355 360 365
 Ala Leu Ser Asn Ala Val Ala Asp Val Ile Asn Arg Arg Ile Gly Val
 370 375 380
 Gly Phe Thr Ser Tyr Glu His Thr Gly Val Pro Val Pro Leu Leu Ala
 385 390 395 400
 Tyr Gly Pro Gly Ala Glu Asn Phe Arg Gly Phe Leu His His Val Asp
 405 410 415
 Thr Ala Arg Leu Val Ala Lys Leu Met Leu Phe Gly Arg Arg Asn Ile
 420 425 430
 Pro Val Thr Ile Ser Ser Val Ser Ser Val Lys Gly Asp Ile Thr Gly
 435 440 445
 Asp Tyr Arg Val Asp Glu Lys Asp Ala Tyr Val Thr Leu Met Met Phe
 450 455 460
 Leu Gly Glu Lys Val Asp Asn Glu Ile Glu Lys Arg Val Asp Ile Asp
 465 470 475 480
 Asn Asn Gly Met Val Asp Leu Asn Asp Val Met Leu Ile Leu Gln Glu
 485 490 495
 Ala

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Pro Arg Asn Ile Ala Ala Val Cys Ala Leu Ala Ala Leu Leu Gly
 1 5 10 15
 Ser Ala Trp Ala Ala Lys Val Ala Val Tyr Pro Tyr Asp Gly Ala Ala
 20 25 30
 Leu Leu Ala Gly Gln Arg Phe Asp Leu Arg Ile Glu Ala Ser Glu Leu
 35 40 45
 Lys Gly Asn Leu Lys Ala Tyr Arg Ile Thr Leu Asp Gly Gln Pro Leu
 50 55 60
 Ala Gly Leu Glu Gln Thr Ala Gln Gly Ala Gly Gln Ala Glu Trp Thr

65					70					75					80
Leu	Arg	Gly	Ala	Phe	Leu	Arg	Pro	Gly	Ser	His	Thr	Leu	Glu	Val	Ser
			85						90					95	
Leu	Thr	Asp	Asp	Ala	Gly	Glu	Ser	Arg	Lys	Ser	Val	Arg	Trp	Glu	Ala
			100						105				110		
Arg	Gln	Asn	Leu	Arg	Leu	Pro	Arg	Ala	Ala	Lys	Asn	Val	Ile	Leu	Phe
		115					120					125			
Ile	Gly	Asp	Gly	Met	Gly	Trp	Asn	Thr	Leu	Asn	Ala	Ala	Arg	Ile	Ile
		130				135					140				
Ala	Lys	Gly	Phe	Asn	Pro	Glu	Asn	Gly	Met	Pro	Asn	Gly	Asn	Leu	Glu
145					150					155					160
Ile	Glu	Ser	Gly	Tyr	Gly	Gly	Met	Ala	Thr	Val	Thr	Thr	Gly	Ser	Phe
				165					170					175	
Asp	Ser	Phe	Ile	Ala	Asp	Ser	Ala	Asn	Ser	Ala	Ser	Ser	Ile	Met	Thr
			180					185					190		
Gly	Gln	Lys	Val	Gln	Val	Asn	Ala	Leu	Asn	Val	Tyr	Pro	Ser	Asn	Leu
		195					200					205			
Lys	Asp	Thr	Leu	Ala	Tyr	Pro	Arg	Ile	Glu	Thr	Leu	Ala	Glu	Met	Leu
		210				215					220				
Lys	Arg	Val	Arg	Gly	Ala	Ser	Ile	Gly	Val	Val	Thr	Thr	Thr	Phe	Gly
225				230						235					240
Thr	Asp	Ala	Thr	Pro	Ala	Ser	Leu	Asn	Ala	His	Thr	Arg	Arg	Arg	Gly
				245					250					255	
Asp	Tyr	Gln	Ala	Ile	Ala	Asp	Met	Tyr	Phe	Gly	Arg	Gly	Gly	Phe	Gly
		260						265					270		
Val	Pro	Leu	Asp	Val	Met	Leu	Phe	Gly	Gly	Ser	Arg	Asp	Phe	Ile	Pro
		275					280					285			
Gln	Ser	Thr	Pro	Gly	Ser	Arg	Arg	Lys	Asp	Ser	Thr	Asp	Trp	Ile	Ala
		290				295					300				
Glu	Ser	Gln	Lys	Leu	Gly	Tyr	Thr	Phe	Val	Ser	Thr	Arg	Ser	Glu	Leu
305				310						315					320
Leu	Ala	Ala	Lys	Pro	Thr	Asp	Lys	Leu	Phe	Gly	Leu	Phe	Asn	Ile	Asp
				325					330					335	
Asn	Phe	Pro	Ser	Tyr	Leu	Asp	Arg	Ala	Val	Trp	Lys	Arg	Pro	Glu	Met
			340					345					350		
Leu	Gly	Ser	Phe	Thr	Asp	Met	Pro	Tyr	Leu	Trp	Glu	Met	Thr	Gln	Lys
		355					360					365			
Ala	Val	Glu	Ala	Leu	Ser	Arg	Asn	Asp	Lys	Gly	Phe	Phe	Leu	Met	Val
		370				375					380				
Glu	Gly	Gly	Met	Val	Asp	Lys	Tyr	Glu	His	Pro	Leu	Asp	Trp	Pro	Arg
385				390						395					400
Ala	Leu	Trp	Asp	Val	Leu	Glu	Leu	Asp	Arg	Ala	Val	Ala	Trp	Ala	Lys
				405					410					415	
Gly	Tyr	Ala	Ala	Ser	His	Pro	Asp	Thr	Leu	Val	Ile	Val	Thr	Ala	Asp

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Tyr	Lys	Trp	Ile	Ile	Glu	Gly	Lys	Leu	Ala	Gln	Ala	Pro	Phe	Pro	
1				5					10					15		
Ser	Leu	Gly	Glu	Leu	Ala	Asp	Leu	Lys	Arg	Leu	Phe	Asp	Ala	Ile	Ile	
			20					25					30			
Val	Leu	Thr	Met	Pro	His	Glu	Gln	Pro	Leu	Asn	Glu	Lys	Tyr	Ile	Glu	
		35					40					45				
Ile	Leu	Glu	Ser	His	Gly	Phe	Gln	Val	Leu	His	Val	Pro	Thr	Leu	Asp	
	50				55						60					
Phe	His	Pro	Leu	Glu	Leu	Phe	Asp	Leu	Leu	Lys	Thr	Ser	Ile	Phe	Ile	
65				70					75						80	
Asp	Glu	Asn	Leu	Glu	Arg	Ser	His	Arg	Val	Leu	Val	His	Cys	Met	Gly	
			85						90				95			
Gly	Ile	Gly	Arg	Ser	Gly	Leu	Val	Thr	Ala	Ala	Tyr	Leu	Ile	Phe	Lys	
		100				105						110				
Gly	Tyr	Asp	Ile	Tyr	Asp	Ala	Val	Lys	His	Val	Arg	Thr	Val	Val	Pro	
	115					120						125				
Gly	Ala	Ile	Glu	Asn	Arg	Gly	Gln	Ala	Leu	Met	Leu	Glu	Asn	Tyr	Tyr	
	130					135					140					
Thr	Leu	Val	Lys	Ser	Phe	Asn	Arg	Glu	Leu	Leu	Arg	Asp	Tyr	Gly	Lys	
145				150					155						160	
Lys	Ile	Phe	Thr	Leu	Gly	Asp	Pro	Lys	Ala	Val	Leu	His	Ala	Ser	Lys	
			165						170					175		
Thr	Thr	Gln	Phe	Thr	Ile	Glu	Leu	Leu	Ser	Asn	Leu	His	Val	Asn	Glu	
		180					185						190			
Ala	Phe	Ser	Ile	Ser	Ala	Met	Ala	Gln	Ser	Leu	Leu	His	Phe	His	Asp	
	195						200					205				
Val	Lys	Val	Arg	Ser	Lys	Leu	Lys	Glu	Val	Phe	Glu	Asn	Met	Glu	Phe	
	210					215					220					
Ser	Ser	Ala	Ser	Glu	Glu	Val	Leu	Ser	Phe	Ile	His	Leu	Leu	Asp	Phe	
225				230					235					240		
Tyr	Gln	Asp	Gly	Arg	Val	Val	Leu	Thr	Ile	Tyr	Asp	Tyr	Leu	Pro	Asp	
		245						250						255		
Arg	Val	Asp	Leu	Ile	Leu	Leu	Cys	Lys	Trp	Gly	Cys	Asp	Lys	Ile	Val	
		260					265						270			
Glu	Val	Ser	Ser	Ser	Ala	Lys	Lys	Thr	Val	Glu	Lys	Leu	Val	Gly	Arg	
	275					280						285				
Lys	Val	Ser	Leu	Ser	Trp	Ala	Asn	Tyr	Leu	Asp	Tyr	Val				
	290					295						300				

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Met Arg Ile Leu Leu Thr Asn Asp Asp Gly Ile Tyr Ser Asn Gly Leu
 1      5      10      15
Arg Ala Ala Val Lys Gly Leu Ser Glu Leu Gly Glu Val Tyr Val Val
      20      25      30
Ala Pro Leu Phe Gln Arg Ser Ala Ser Gly Arg Ala Met Thr Leu His
      35      40      45
Arg Pro Ile Arg Ala Lys Arg Val Asp Val Pro Gly Ala Lys Ile Ala
      50      55      60
Tyr Gly Ile Asp Gly Thr Pro Thr Asp Cys Val Ile Phe Ala Ile Ala
      65      70      75      80
Arg Phe Gly Asp Phe Asp Leu Ala Val Ser Gly Ile Asn Leu Gly Glu
      85      90      95
Asn Leu Ser Thr Glu Ile Thr Val Ser Gly Thr Ala Ser Ala Ala Ile
      100      105      110
Glu Ala Ser Thr His Gly Ile Pro Ser Val Ala Ile Ser Leu Glu Val
      115      120      125
Glu Trp Lys Lys Thr Leu Gly Glu Gly Glu Gly Ile Asp Phe Ser Val
      130      135      140
Ser Ala His Phe Leu Arg Arg Ile Ala Thr Ala Val Leu Lys Lys Gly
      145      150      155      160
Leu Pro Glu Gly Val Asp Met Leu Asn Val Asn Val Pro Ser Asp Ala
      165      170      175
Ser Glu Gly Thr Glu Ile Ala Ile Thr Arg Leu Ala Arg Lys Arg Tyr
      180      185      190
Ser Pro Thr Ile Glu Glu Arg Ile Asp Pro Lys Gly Asn Pro Tyr Tyr
      195      200      205
Trp Ile Val Gly Arg Leu Val Gln Glu Phe Glu Pro Gly Thr Asp Ala
      210      215      220
Tyr Ala Leu Lys Val Glu Arg Lys Val Ser Val Thr Pro Ile Asn Ile
      225      230      235      240
Asp Met Thr Ala Arg Val Asp Phe Glu Asn Leu Gln Arg Leu Leu Ser
      245      250      255
Leu

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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Met Glu Asn Leu Lys Lys Tyr Leu Glu Val Ala Lys Ile Ala Ala Leu
 1      5      10      15
Ala Gly Gly Gln Val Leu Lys Glu Asn Phe Gly Lys Val Lys Lys Glu
      20      25      30
Asn Ile Glu Glu Lys Gly Glu Lys Asp Phe Val Ser Tyr Val Asp Lys
      35      40      45
Thr Ser Glu Glu Arg Ile Lys Glu Val Ile Leu Lys Phe Phe Pro Asp
      50      55      60
His Glu Val Val Gly Glu Glu Met Gly Ala Glu Gly Ser Gly Ser Glu
      65      70      75      80
Tyr Arg Trp Phe Ile Asp Pro Leu Asp Gly Thr Lys Asn Tyr Ile Asn
      85      90      95
Gly Phe Pro Ile Phe Ala Val Ser Val Gly Leu Val Lys Gly Glu Glu
      100      105      110
Pro Ile Val Gly Ala Val Tyr Leu Pro Tyr Phe Asp Lys Leu Tyr Trp
      115      120      125

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Gly Ala Lys Gly Leu Gly Ala Tyr Val Asn Gly Lys Arg Ile Lys Val
 130 135 140
 Lys Asp Asn Glu Ser Leu Lys His Ala Gly Val Val Tyr Gly Phe Pro
 145 150 155 160
 Ser Arg Ser Arg Arg Asp Ile Ser Ile Tyr Leu Asn Ile Phe Lys Asp
 165 170 175
 Val Phe Tyr Glu Val Gly Ser Met Arg Arg Pro Gly Ala Ala Ala Val
 180 185 190
 Asp Leu Cys Met Val Ala Glu Gly Ile Phe Asp Gly Met Met Glu Phe
 195 200 205
 Glu Met Lys Pro Trp Asp Ile Thr Ala Gly Leu Val Ile Leu Lys Glu
 210 215 220
 Ala Gly Gly Val Tyr Thr Leu Val Gly Glu Pro Phe Gly Val Ser Asp
 225 230 235 240
 Ile Ile Ala Gly Asn Lys Ala Leu His Asp Phe Ile Leu Gln Val Ala
 245 250 255
 Lys Lys Tyr Met Glu Val Ala Val
 260

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGCCCCAGCG	TGTTGCCAAG	ATGCTTGAAA	GAATGCTATC	CAAGGCGGAA	TCTATGCTCG	60
GCGACGCCCA	GAGGCTTATC	GAGGAGGGTA	AGGCCGTTGA	GGCTAAGAAG	CTGTTAGCGG	120
CTGCTCATAG	GCTAGTAGAT	CGCCTAGAGG	ATGCTCTCGA	CCACGCCCTC	AACCATATAG	180
AGCATCACAA	GGAACATCAT	GAGGAGCACC	ACAAGGAGCA	CGACTAACAA	CACTCTTAGA	240
ATCTCGAGAC	GAGCTTGCTT	CCCGTGTCTC	TCGCGCCTAG	CCAGTTTTTA	ATAGCCTAAG	300
CCGAGACCCA	CATTCCAACA	TACTCCGTT	TGTCATATC	ATGTTCTAAT	TGTCACACCG	360
CCCGTATAAA	TTGGGGGACC	TGGAGGAAGC	GTTGCCGGTG	ACCCCGCGTG	GCCAAGAAGG	420
CTGTCTGCCC	AATATGCGGT	GGCGATGTTG	AACTACCCGA	TAACGTAATG	GATGGCGAGA	480
TCGTGGAGCA	CGACTGTGGG	GCAATGCTAG	TCGTGAGGAT	CCGGGATGGC	AATGTTGTTC	540
TAGAGCAGTT	GGAGCGCGTT	GAGGAGGACT	GGGGAGAGTA	GAGGCTATGC	GCATAGCAAT	600
CGTTTTATGAC	CATCCGCGTG	TTGAGGAGAA	GAGGTTAGCT	GAGGAAGCGA	GGAAGCTTGG	660
TCACGAACCT	GTCTCTTTTA	ATATTGACTC	GTTGCTCTTT	CGCCTTGATA	GCCTGGAGCG	720
CATTCTAGGC	GATGTTGATG	TAGTACTTCA	GAGGGCGGTG	AGTTACTTCA	AGGCTCTCGA	780
GTCTACAAGG	ATACTCGAGG	CTGCCGGCTA	CACTGTCATC	AACAATAGTT	TAGTGCAGCT	840
TAACTCGGGC	GACAACTAT	TGACAACGAT	CTTGCTTGCT	AAGCATGGTG	TGCCAACACC	900
GCGTGCATAC	GCTGCTTTTT	CGCGTGACAC	TGCTGTGCGG	GCTGCAGAGG	AGCTTGGATA	960
CCCCGTGTGT	GTCAAGCCCG	TCATTGGTAG	TTGGGGTAGG	CTTGTGGCTA	GGGCTGATTC	1020
CAGGGAGAGT	CTAGAGGCTG	TGATAGAGCA	TAGAGAGGTT	CTCGGCCCGG	CTTACTACAA	1080
GGTTCATTAT	GTGCAAGAGT	ATGTGCGCAA	GCCTCTACGT	GACATACGCG	TATTCGTGAT	1140
TGGTGATGAG	GTTCCTCGTG	CGATATACAG	GGTTAACGAG	CGTCATTGGA	AGACTAACAC	1200
GGCACTAGGC	GCCAAGGCCG	AGCCTGCGCC	AGTGACCCCC	GAGTTACGTG	AGTTAGCGCT	1260
TCGCGCGGCC	AAGGCTGTGG	GTGGCGGTGT	GCTTGGTATA	GATGTGTTTG	AAGACCCGGA	1320
GAGAGGCCCTC	CTCGTGAACG	AGATTAACGC	GAACCTCGGAC	TTCAAGAACA	CTGAGAGGGT	1380
GACCGGGTTT	AACATGGCTA	GGGCTATCGT	CGAGTATGCA	GTGTCGGTCG	CGAAGAGGTG	1440
AATGGAATGG	ATAGGGTAGA	GGTGCTTCTG	GATGAGGCTA	GGCGTGGCGC	TATAGAGGGT	1500
GACGCTCGCC	CGCATGTGA	AGCGGCATTA	AGGCTGGTTG	ACGTTGTGCT	CCGCGAGGGG	1560
CCTAGGGTTG	CACAGGAGTC	TGGGCGTGGG	ATTGAACCCG	GTGATGTACT	ACTAGCTGAG	1620
GCTCTGAGCT	TGAGAGCAGA	GCAGGTGAAG	GAGGAGCCCA	AGGCGGACAA	TTGTCTGGAG	1680
CTCGCAAAGG	CTGCATTCCG	CCTCTATAAG	CGGCTCCAGG	GGATGGAGTA	AAGTTCGCAG	1740
TGTGTTGCCC	GTTTTAGCCT	CTGCCTTACT	TTCTACTCGC	GTGAGGCGAG	TGTCCCTTGA	1800
CACGTTGCTG	GCGCGAGCTG	AGAAACGACC	TCGAGATGAT	ACCCGAGATC	GTCGAGAAGC	1860
AGATCGAGGA	GACGATAGTG	CCGAGGGGTC	TTGGCGAGCA	ACGACTTGTG	TTCATTGGCA	1920
GCGGTGATTC	TTTCGCGGCC	GCACTTGTAG	CCGAGCATGC	CGGCATAGGC	GTCGCACGCG	1980
ATCCTCTTGA	TGTGCTAGTG	GCTGGCGTTG	ATGGGCCTGG	CGACGCTATA	CTCCTAAGCG	2040

TTGGTGGGCG	CTCAAAACGA	GTTGTTGACG	CGGCTCGTTT	CCTGTCTTCA	CGTGGCTTTT	2100
GTATCATAGC	GGTCACGGGT	AACGAGAGGA	GTCTCTCGC	ACGCACAGCA	CACGTTACCG	2160
TGAAGCTCGT	CTATCTGAC	CTCGCTGTG	GCATGGGCGC	CGCACGCCAT	GTGCTATGC	2220
TTGCAGCGCT	CTCCGCATTG	TTCAACGCTA	GACCTCGTAT	ACCCGAGAAG	CTTGTTGAGG	2280
AGCCCCCTGCC	TTTCGACCCT	CAGGCTGTGT	ACGCGGGTGT	GGGCGTTGGT	GTAGCCTCTG	2340
CCCTGTTTCAT	GGTGTGAAG	ATCTGCGAGT	TGCTGCGAGA	CTGCGCCACC	TGGTGGCATC	2400
TAGAGCAGTT	CGCACACGCA	CCTGTCTATG	GCACGAGAAG	CAATATACTC	GTGCTGTATC	2460
CGATCCTCGT	TGTGAGAGGA	GCACGCTAGA	GGAGTATCTC	TCGGCCTTCC	GGGAGGCCGG	2520
GTTTGAGGTC	ACCACTGTAC	CCGTGTTGAA	CGACCCTTGG	TCTACAGCTA	TTCTCCACGC	2580
TACGCTGGCC	ATCTCCAGTG	CTGCAGAGAC	CGCCTTCAGT	CGCGGCATTG	AGGAGCCGGG	2640
ATATCGTGCA	CATCCCGCGC	TTAGCAGGCT	AACCAGGCTG	ATCTACCTAG	AGGAGTAGAA	2700
CCTCTCGAGG	ACCGGTATGT	AGTGGTCTAG	AAGCTTCCCG	TCATGGTGTA	TCGCGAGGCC	2760
TATTCCTGCT	CTCCTCGCGC	CTTCCACGTT	GGGCTCATAA	TCATCTATGA	ATGCTGTTTT	2820
CGCTGGGTCC	GCGCGAAGGA	GTTGCATCGC	CGCCTCGTAT	ATCTTTGTGT	GTGGCTTGCA	2880
AAAGCCGACA	ATATCCCTCG	TAACCACCGT	ATCCACGAGG	TGGGCTAGAT	CGTCACGCTC	2940
TAGAAGTAGA	CGTACGCATT	CGTAGCACCA	GTTGTTGAG	ACTATGCCGA	CCAGTATCCC	3000
GTTTCTCTTG	GCCCATCTTA	GCAGCTCGTA	TGTACCCGGT	GCTACGTATA	CGCCAGACAG	3060
CACAGCTGAT	TGCAATACCC	TTGCTAATGC	CTCTGCCCTT	GAGGGGGTCG	GCGTCAAGCC	3120
GTGTTTTGCG	AGGAGCACGG	CAGCCGCATA	CACATATACT	TGTTGCACGG	AGACATCCAG	3180
CCTCCACGTG	TCCATTACAC	GCCTCACGCT	ATCCGGCGTC	GCGTCGGCCC	CTAGGGCACG	3240
TAGATGTCTG	GCAGCAGTCT	CGTAGAGAGT	CTCTCGTAC	CACTCATTTG	TGAGGTAAAT	3300
GACGCCACCT	AAATCCAGCA	GGAGTGTAGG	GTTACGCGGC	AAGGCGCCTC	CTCATGTATT	3360
CGAGGAGGCC	GCCCGTTGCC	AGAATTTTCA	CTACAACACC	CCGGAAGGGC	GGGAAACGGT	3420
ACGTCAACAC	CCTACCATCC	TTCTTGATGA	GCTTCGCTAC	ACCCTCGTCA	AGGTTTATCT	3480
CTATCTCGTC	GCCCTCCTCG	GCCGCCTCCA	CGAGCTCTGG	GAGCACTATA	ACGGGGAGCC	3540
CGTTGTTAAT	CGCGTTACGG	TAGAATATTC	TCGAGAAGCT	CTTCGCTATG	ATGGCCTTGA	3600
CGCCTGCAGC	CTTGAGAGCT	ATCGCGGCTT	GCTCCCTGCT	ACTACCCATA	CCAAAGTTCC	3660
TACCCGCGAC	CAGCACTACA	CCCTTGAGCG	CCTTCTTGGG	GAACCTCCGA	TCCAGAGGCT	3720
CCATAGCATG	CTCGGCAAGC	TTCTCCGGCT	CAGTATATAC	CAGGTAGCGG	GCAGGGATAA	3780
TCACGTCGGT	GTTGATGTTA	TTGCCGTAAT	TGAGCACAGG	GCCCTTCACG	ACACCCAGGT	3840
TTCAAGAGAGG	TTCAACCACAA	GTTTGGCCTC	GCTATCCAG	GCTATAATCC	AGCTGTTTAC	3900
TCGGCCAGCT	TCACCCACAC	ACTTTTCAAC	TCCATTATCC	TTGTAGCGCA	ATCTACCCTT	3960
CTGGGTAGCA	CAGCGTTAAG	CCCATAGTGC	CAAGGCGCCA	CAATGATGCC	CTCCGGCACA	4020
TTCTCGTCCG	GTATCAGCCG	GAGGCGTATG	GCCCCTCTCT	CCGTCTCGAG	CCTAGCGTGA	4080
CCGGCGCCAG	CCTCCTTAGG	GTTGACTCGT	GCGTATAGCT	CGCCGCTCAC	ATCTAGCATC	4140
CGGTTTGATC	AGTAGCTCAC	CGGGTCTCTT	GCAGTCACGA	GCACCTTCCT	ATCACCATCG	4200
GGCACGACCG	GCTCGACCGG	CGGGTATAGA	CGGACGCGTA	TCCTCGAGAC	ACGCCTGGGC	4260
AGGAGGTACT	CGCCTCTCTC	CGCAACCGCC	TTGGAGGAA			4299

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGACTGATA	AAGAAAAAGA	AGAGGTTTAA	GGGCCTCAAT	ATTAAATTCT	ACACATTAGA	60
TATCCAAAAT	GGAGAATTAC	TTAATCTAGA	GACTTACCTT	AAGGAGTTAC	ATGAGTTTCT	120
TAGAGGCCCT	ACATTAAAAA	GAAAAGTAGA	AGAGGAACAA	TGACCCCGGA	AGAGCTCCTA	180
ACCCGCCTCG	AATTCAAAGG	AGTAACCCCT	GAAAAGATGC	TCAATACTGC	GTTAGAGCTC	240
TACATCGGCG	ACGAGCGCGA	GAAAGTTCGA	GAAAGGCTGA	GAGAGCTGAT	GCTGAGGTAT	300
CTGGGCGACA	TCAACGTTCA	AGCTCTGCTC	TTTTCGGCTC	TACTGCTCGA	AGAGAACCTT	360
AAGGTTGAGG	GCGACCCCGT	GAACCTTGTC	GCCGACGAGC	TCATCGGCAT	GAACATCGCC	420
GAGCTCATAG	GTGGAAAGAT	GGCGCTCTTC	AACTTCTTCT	ACTACGACAC	CAAGAAGCCC	480
GGCATTTTAG	CCGAGCTTCC	GCCTTTCCTC	GACGATGCGA	TAGGGGGGCT	TATAGCGGGC	540
TGTATGACAA	GGCTGTTTCA	GGGGGTGTAC	GGTGCGGAAT	CTCTTACCCT	TCTTCACGCG	600
GATTCCGGTC	AAAGGCAACT	TCAAAAGGGT	TAGAAATGAG	CTCTGGGCAC	TTCCCATTCT	660
CGCACCCGTA	ACTTCGGCCC	TGGCGACGCT	CGTGGGCTCT	GTGCTCGCCG	GGGTAATAAT	720
CCTGGGCGGC	AACTACGCGT	TTCACCCAAC	GTCTCGGCAA	CCACGCTGCT	GATAACCCTC	780
ATAGGCTTCG	TCGTGGTCTA	CAGCATACTG	TTCTACATCT	GGCTCCACTT	CGTCAGGAAG	840

CTCATCAGGG	AGGGCCCCGA	ACCGGTTGAG	GGTGACGTCA	CCGCGAAGCC	GACCCCTGCC	900
GTTAGCGCCG	CGGGAGGTGG	TCAGTGATGG	ACTACGCGAC	CGCATGGTTT	TACTTCTCCG	960
CCTTCCTCCT	CGGAATGTAC	TTAGCGTTTG	ATGGCTTCGA	CCTTGGCATA	GGCGCGTTGC	1020
TCGCCCTGAT	TAAGGACCAG	AGGGAGCGCG	ACATACTCGT	GAACACCATC	GCGCCGGTCT	1080
GGGACGGCAA	CGAGGTCTGG	TTCATCACCT	GGGGTGCCGG	GCTCTTCGCG	ATGTGGCCGG	1140
CGCTCTACGC	GACGCTCTTC	AGCACGTTCT	ACCTTGCCGT	CTGGCTGCTC	GCGTTCCTGT	1200
TCATATTAG	GGCTGTCCGC	TTTGAGTTCA	GGAACAAGAA	CAAGGAGCTA	TGGGACAAGC	1260
TCTTCGCTCT	CGTCAGCGCG	TTAATCCCCG	TCGTCATCGG	CGTCATAGTC	GGCAACCTCA	1320
TCATGGGAAT	TCCCATTGAC	GCCAAGGGCT	TCCACGGCTC	ACTGCTGACG	CTCTTCAGGC	1380
CCTACCCGCT	CATCGTCGGC	CTCTTCATAC	TCTTCGCGGT	GACCTGGCAC	GGAGCCAACT	1440
GGGGCGTCTA	CAAAACCACA	GGAAAGCTCC	AGGAGCAGAT	GAGGGAGCTC	GCCTTCAAGG	1500
CCTGGCTCCT	GACCGTCGTC	TTCCTCCTGC	TCACAGTCAT	CGGCATGAAA	ATCTGGGCCC	1560
CACTGAGGTT	CGAGAGGGCA	CTAACGCCGC	TTGGGCTCCT	CCTAACGGTT	GTCATCCTCG	1620
TGGCAGGACT	GCTCGACGGA	CAGCTCATCA	AGAAAGGGGA	GGAGAATTTG	GCCTTCTACA	1680
TCAGCTGGCT	GGCCTTCCCG	CTCGTTGTGT	TCCTCGTCTA	CTACACAATG	TACCCCTACT	1740
GGGTCATCTC	GACCACCGAT	CCGAACCTCA	AGCTCAGCAT	ACACGACCTC	GCGGCATCTC	1800
CGCTGACCCT	CAAGGCCGTC	TTGGGAATCT	CGCTGATCCT	GGCGGTCATC	ATCATGGCCT	1860
ACACCCTCTA	CGTATACAGG	GCCTTCGGCG	GAAAGGTCAC	CGAGGCGGAG	GGCTACTACT	1920
GAGTTCCCCCT	TTCCTTTTTTC	GATATTCGAA	CTTTTTTAGG	GAAAAGTTTA	TAATTTCGAGT	1980
CACCTAAGTT	CCTTCTGGAA	ACCTAAAAAA	CGGTGGTTCGA	AATGCACAGA	GGCAGATCTA	2040
CCGGCTGGCC	CTACGACCGG	AAGCCGGTCC	TCGTCTTCTG	GGAAACCACC	AAAGCCTGCC	2100
GGCTCAAGTG	CAAGCACTGC	AGAGCGGAGG	CAATACTCCA	GGCACTGCCG	GGCGAGCTGA	2160
ACACGGAGGA	GGGAAAGGCC	CTCATCGATT	CCCTCACCGA	CTTCGGGAAG	CCCTACCCGA	2220
TACTCATTCT	CACCGGTGGC	GACCCGCTCA	TGAGGAAGGA	CATCTTCGAG	CTCATCGAGT	2280
ACGCCGTTGA	GAAGGGCATT	CGCGTTGGTC	TCGCCCCCGC	TGTAACGCC	CTCCTGACCG	2340
AGGAACAAT	CGAGAGAATC	GCGAGGAGCG	GAGTTAAGGC	GGTAAGCATA	AGCCTCGACA	2400
GCCCGTTTTCC	AGAAGTTCAC	GACGCAATCA	GAGGCATAGA	AGGGACGTGG	GAGAAAACCG	2460
TCTGGGCCAT	CAAGGAGTTC	CTGAAACACG	GCCTAAGCGT	TCAGGTGAAC	ACGGTTGTGA	2520
TGCGCGAGAC	CGTTGAAGGA	CTGCCCCGAG	TGGTGAAACT	GCTTAAAGAC	CTCGGCGTCG	2580
AAATCTGGGA	GGTCTTCTAC	CTCGTCCCCG	CCGGGAGGGG	CAACTTCGAG	AGCGACCTGA	2640
GGCCGAGGA	TGGGGAGGAC	GTCAACACT	TCCCTACGA	GGCCTCGAAG	CACCTCCTCG	2700
TGAGGACCAC	CGAGGGCCCC	ATGTTCAGGC	GAGTGGCGAT	AATGAGGAAA	GCCCTTGAGG	2760
AGAAGGGATT	CGACCCCGAC	GAGGTTCTCA	AGCCCGGGGA	GCTCTACTTC	CGCTGAAGA	2820
AACGGCTCGT	TGAGCTTCTC	GGCGAGGGGA	ACGAGGCGAG	GGCCCAAAT	ATGGGAACGC	2880
GCGACGGGAA	GGGAATAGTC	TTCATCGCCT	ACAACGGCAA	CGTCTACCCG	AGCGGTTTCC	2940
TGCCCTTCAG	CGTCGGCAAC	GTCCGCGAGA	AAAGTTTGGT	TGAGATTTAC	AGGGAGAGTG	3000
AACTTATGAA	AAAGCTCCGC	TCGGCCGAGT	TCGAGGGGCG	CTGCGGGAGG	TGCGAGTTCA	3060
GGGAAATCTG	CGGGGGAAGC	AGGGCGAGGG	CCTACGCCTA	TCGCTTAAAC	CCGCTCGCCG	3120
AAGACCCTGC	CTGCCCCTAC	GAGCCGGGCT	CATACCTAAG	GCTCGCCAAA	AAGTTCAATC	3180
TTCACCTTCC	GATTGAGATT	TTTGGAGCCC	AAAAGCCGAT	TTGAGGTGAT	GGAAATGAGG	3240
TGGAAGGCTG	TTTTACTGAT	TGGAATCCTC	CTCGTGTCTG	TCCTCGGTGC	CGGATGCGTT	3300
GGCTCGAATA	CCTCAACTGA	AACCGGCCCA	TCCCAGAAGG	AAATAACCGT	GAAGGACTTC	3360
TCGGGAAGGA	ACATCACGGC	TAAAGTTCCG	GTTACGCGGG	CGGTCGTTCT	CTCGACTTCC	3420
GCCCTCGAAA	TAATCCAGCT	CCTCAACGCG	AGCGACCAGG	TCGTCGGTAT	TCCAAAGGAG	3480
GCCAGTACG	ACGCTTTACT	GAGCGAAAGC	CTGAAGAACA	AGACCGTCGT	TGGCGCGAGG	3540
CTCAAGATTG	ACGACTGGGA	GAAGGTTTTA	GCCTTAAAGC	CCGACCTAAT	CATCGACCTC	3600
GACCTGAAGA	AGTTCTACAA	CGTTGACGAG	CTCCTCAACC	GCTCCGCCAG	CTACGGAATT	3660
CCGGTCGTCC	TGCTGAGGGA	GGATAACCTT	GAGGACATAC	CGAAGGCGGT	TTGCTCCTC	3720
GGTCAGCTCT	TCGGAAGGGA	GAAAGAGGCC	AAGGCCTTCG	ACGACTACTT	CAACGAGCAG	3780
GTGAAGGAGG	TTAAGGCCAT	AGCCTCAAAG	ATTCCAGCGG	AGGAGAGAAA	GAAGGCAGTA	3840
ATGATACAGC	CGATAATGGG	CAAGCTCTAC	CTCGTCAACG	GCAACGACGT	CCTTGCTCAG	3900
GCCGTCAGGC	TCGTTGGGGC	GGACTACCTC	GTGAACCTGA	CCTTCAACGG	CTACACTCCG	3960
GTTAGGGTCC	CGATGGACGG	GGAGAAGATA	ATAGCGAACT	ACCGCGATGC	AGACGTCGTA	4020
ATCCTCCTGA	CGAGCGCCGT	AACGCCTTAC	GACCAGGTTCG	AGAAGCTCCG	GGAGGAGATG	4080
CTCAGCGACG	AGGCCTGGAG	GGGCATTAAG	GCCGTCAGGG	AGGGCAACGT	AGTAATCCTC	4140
AGGGCGGACA	TGGGTAAAGA	CTCCTTCCTC	CGCTGGAGCC	CGCGCTTGGC	AGTGGGAATC	4200
TGGGTCATTG	GAAAGGCAAT	CTACCCGGAC	TACTATCCTG	ACTGGAACGA	CAAGGCCAAG	4260
GACTTTCTGA	AGAGGTTTTA	CGGCCTCTCC	TGATTTTTCT	TTTGGGGTGG	GACGATGATA	4320
GCGGTCTTTC	CAGCGAGTCT	CGCGGAAATC	GCTCAAACCTG	TCGGGAAAGC	CGGGGAGATA	4380
GCCGAGTGA	ACGAGGAAAT	CAGGTTTCGAC	CCCTGCTGCTG	CGGAGCTGAA	GGATAAGCCT	4440
GTACATCGGAA	AGTACCTCAA	GCGGAGCAAG	AGGACCTACT	GGGACGTTTT	AGAGGAGCTT	4500
AGGCCGGACC	TTATCCTCGA	CTTCGATGTT	GAGAACCTGC	ACTCCGGGGA	CGAGCTGAGG	4560
GCCTTTGGGG	AGCGTATAGG	GGCAAGGGTC	GAGCTGATTG	ACTTCGAGAC	CGTTGAAGGC	4620
TTCGTCGAGG	CGAGCAGGAG	GATAGCCGAG	CTAACGAGGG	GCGACTTTTC	AAAGCTCGGC	4680
GGTTCTATG	AGAAGCACCT	GACGAGGCTG	GGTGAGATAA	CTGAAGCCAT	CGAGGAGAGG	4740

CCTAAAGCCC	TGCTCACCTA	CCGGAACCTTC	AACGTCGTAA	CGAGGACCAA	CGTTCTGAGC	4800
GACGCGGTTA	GAAAAGCAGG	GGCGATGAAC	CTCGGCGAGA	GGATACGGAC	AAAGCGGAAG	4860
GTCTATCCGG	TAAAGAAGGA	GCGCTTCTTC	AGTCCCTTCG	GCGATGCGGA	GCACCTCTTC	4920
CTGCTCACGA	GCATAATGAC	GGACAGGGAG	AAAATGGAGG	GGATAAGGGA	TGAAATCCTT	4980
GACTCGGCCG	AGTGGAGGGC	AATGGAAGCC	GTTGAGCTCG	GAAACGTGCA	CATAGTTGGC	5040
TCGGCCCTCG	ACCTTGAGAG	CTTCATGCGC	TGGAGTCCCC	GCATAATCCC	GGGAATCTAC	5100
CAGCTTGGA	GGTTTATACA	CGGAACAAAT	CACCCACGAA	TCTCGTGGAA	ATCACTGCAA	5160
AAGTTTAAAA	TCCCCCTCCC	ACCCCTCGAA	GAACAAAAAC	GCATCGTCGC	CTACCTCGAC	5220
TCGATACACG	AGCGCGCCCA	AAAGCTGGTA	AAGCTCTACG	AGGAGCGGGA	GAAGGAGCTT	5280
GAGAAGCTTT	TCCCCGCGGT	GCTTGATAGG	GCGTTTAGGG	GTGAGCTGTG	ATTCCGGGAA	5340
TGGAATACGG	CTTTGAGAGG	GCAATCTTTG	AGATAGTCAG	CGGCTTTGTT	CTCTCCCTCG	5400
TAGTCAGGGC	TTTCGCTTAC	AGTTTGGTTC	TTCCATGGGT	ATCCTTTTTG	TTCAACGTTT	5460
TTTCGATACT	TCTGACAATA	GGCCTGATTG	ACAAAATGCC	CTTCTGGTCC	ATGTCATATC	5520

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCTTGATA	TCGAATTCCT	TATATGAAAA	ATTCATCGAA	TTGGTAAAAA	ACCACGATCT	60
TCATGTGGAA	ACTGGAATAT	TTGCTGCGCA	TATGCTTGTG	GAAATACATA	ACGATGGTCC	120
GGTGACTTTG	TTACTTGATT	CAAGAAAAGG	TATTTTGAAG	TCATCTTTGC	TGTCTCTAGG	180
AGGACTATAT	GCCTGAATAC	TCGCATAGCA	ATAAAAACAA	CTTTTTTGCC	GAAAACGATG	240
TGAAGAATTG	TCATCTACTG	CATGTATGTT	GTGCACCCGA	TTGGCAATT	TCTTATTTGT	300
CCGGTGCACG	TGGTGATATT	TTCTTTTACA	ATCCTAACAT	ACATCCAAAA	GCTGAATACG	360
AGAAACGACA	CGCCGAAGTG	ATTAAAATTG	CTGCACTCTT	TAAAATGAAT	GTTCGAAAAG	420
TTCCTTATAA	TCCTGACCTG	TTCTTCAAGC	TTACTAAAGG	ATTAAAAAAT	GAACCTGAAG	480
GCGGGACAAG	GTGCGAGATT	TGTATAAGAA	TGCGACTAGA	AAAAACAATG	GAATACGCGA	540
AAGAAAATGG	CTACAAGAGT	GTTTCCACAA	CGCTAACAGC	CTCTCCAAAG	AAAAATGTAG	600
CGATGATTGT	GAAGATAGGA	AAAGAACTGG	AAAAAAAATA	CGGTGTGGAA	TTTTTGCCTA	660
ATGTGTACCG	CAAAAGTCCG	CTTTACAACG	ATGCGCAAAA	GCTTATAACG	AAAAATGGGT	720
ATTTACAGAC	AAAACTACTG	TGTTGTATT	TTCTCAATAA	GAACCTCCGT	TATAGTAGCC	780
ACTCAAGAAA	CTAAAACCGT	AAAAAGTGGG	GTGGAAGTAT	GAAAATATAC	CACAAATTAG	840
AAGAAGTTGA	AGAACATAAG	CGGTGCTATG	CATCAATTGC	TTTTTCATCG	AAAGTCAGGG	900
TTGAATATGA	ACATGCTGGC	GAAAAACTTG	CCCTCATCCC	TGTAACCTAT	GGAGACCTTA	960
CGGTGGTTAT	CGAAATTGAC	GATGATAGAG	AAGTATTCAA	TACTTTGTTG	AACGAGCACA	1020
TCAAAAACCTC	TATCCTGAAA	CAGTTTCCGT	ATCCGGAAGA	GATTAGAGGG	TTAGCCAGAC	1080
ATTTTCGCAC	AGAATTGAAG	AATTTAGAAA	TCTGGTTGT	AAAATACAAT	AGTGTGGAAG	1140
AAAAGGAATT	CTCAAGGTAT	TCACTGTCTA	ATATAACATT	CGGTGTGGTG	TCATACAATA	1200
AATTTGATGT	CCATTTGTTA	CCAAGTAATG	TAAAAGTCAG	ACCGAAGCCA	GGATACTGTC	1260
TTTCACATGT	TGTCCAAAAG	CCTGAAGAAG	GTATCAGGCA	AGCATTCTTG	TTAGCCCGGT	1320
GGTTTGGTGG	TGGAAGCTAC	GACCAACTGC	CCAAATTAGC	GCTTGAAAGC	ACTGACATTG	1380
ACCTTGGAAG	GTGGACAAAT	ATAGTCAAAT	ACATCGTTCT	GTGAGATTTT	GAAAAGAGGT	1440
ATTTTTCTGG	TATAATAAAA	AAGCTAAACG	AATTTAGAAG	CGAGACATAT	TTTGACCCAT	1500
TTGCTAGGCT	TGAAATGATA	TCACCTGGCA	TAATACTCGC	CAAGTCAGAG	GGAGGAGGTA	1560
ACTTTGAACC	AGACAGTTAC	GATATCATTT	AGAGCACTTA	CTGAAAATAT	AAAAATTAGCA	1620
CGAGTTGTTA	TACATACTTT	TCTAACATTC	CGAGGAGTGT	TCGATAAAGA	TATATTCGAT	1680
ACGGAATTGG	CTGTAAACGA	AGCGATTGCA	AACATTATTC	AGCATACATA	CAAAGGTGAA	1740
CCAAACTACG	TGTGATGAC	GCCTAATTGG	ATAGAACCAG	ATACACTCGA	AGTGTACTCT	1800
CGCGATTTTG	GTCCAAAAGT	GGACCCAACG	AAAAACAAC	CACGAGATTT	AGATGATATC	1860
AGACCAGGAG	GACTCGGAGT	TTATATAATT	CAACGCATCT	TCGACATTAT	GGAATTCGGA	1920
AACGTGAGTC	ATGGAAATTT	ACTTTATCTA	AAACGCTCCT	TCTTAATACC	TCCTAAAAAG	1980
CAGGAGCTTG	GGAAATTTAA	TAATGAACCC	TATCGAGAAT	ATTGAAAAAA	CCGTCAAAAC	2040
GGGGGAAAGA	GAGCAAAATGG	GCTTGCTCAC	AGGTTTGACA	AAAAATCCAT	CTTTTCATGTC	2100
TGCATTTTTT	GGCTTTTTTG	CAGCACAATT	TTTGAAAGTG	GTGATATACA	AAGATTTCCG	2160
CGTATTTGGT	AGATACGGTG	GTATGCCAG	TGTCATGTT	GCAACAACCT	CAGCATTAGC	2220
TTGGGCTGTT	GGTTACACTA	CAGGTTTGA	TTACCCGCTT	ACAGCCATCG	CTGCAATTTT	2280
CCTTGCTATT	ACAACAGCTG	ATGCTGTTGG	TTTACGAAGA	AATGTCGACC	CCAATAAAGG	2340

ACATACACTA	ATGGAAGCTA	TCTATGGCTT	CTTACTTGGG	TGGATAGTCG	CTCTGCTTAC	2400
GGTTAAGTTG	TATCGATAAT	TTTGAATGAG	TTGTAGTGAA	ATAGCCCAAG	TCTTTTTTTCG	2460
CAATTACATC	ATAATGCCAG	GAGGGTAATT	TACAATGTTT	TTTAGATTAC	CATTTAAAGT	2520
TTTTGTTTTT	GCAGTTTTGT	TGCTTGCCAT	CTCGTTAACA	AGTGTGTTA	GTTTTGGACA	2580
AGATGATGAG	CAGATAAAAA	CACCAAAATTG	GTTTAGAAGT	GCGGTGATTA	AGAAAAAGAGC	2640
TGGTATGAAT	CTAAAGACCG	CCCCAGAGTT	TGTAGATGAC	CTATGGAATG	CGATATACAC	2700
TATAGGCACA	AAATACAACG	TTCCCCCAAC	GCTTATAGCC	GCTGTCATTT	CTGTAGAAAG	2760
CAACTTCGCC	AACGTGAAAG	GTGCTGGAGA	CGTGGTAGGA	ATGATGCAAA	TTTCTATCTC	2820
CACAGCCAAA	AATATATCGA	AACTCCTCGG	CCTCGAACAA	CCAAAAACG	GTTGGGATGA	2880
GCTCCTCACA	AATTATTGGT	TGAATATAAC	TTACGGTACC	GCATACATCG	CTTATCTTTA	2940
CAAAAAGCAT	GGAACCTTAC	AGAAAGCGCT	CGAAGAATAC	AACAACGGAA	AAAATAAAAC	3000
TAAATACGCC	CAGCTGATAC	TACAACAATA	CAACCTATAC	GAGAGCCTCC	ATTCTGCTGA	3060
AATAAGAAAT	AACCAGCAAT	TGGATACAGA	TAATCTTTCG	ACATCTTCTG	AAGCAACAGA	3120
TACTTTGAAT	ACAACCAGTG	CAACAAATTC	ACAACCAACA	TCAGATGCAT	CAAATACATC	3180
AGTTAACACT	TCAGAAATCA	AGTTCCCGCC	TCTTTTCGGA	GTTGCAGGTT	ATTAAGATAT	3240
TTGTTCCGTA	TGTACTTAGG	AATGTGGGGT	GTATAGTTTG	GAAGATGAAA	AAATGAAACC	3300
TGAAACGATA	GTA AAAATTG	AACATTTATC	TTTTTCTTAC	CCGAGTTTCA	GTCTCAAAGA	3360
TGTAAGTTTT	GAGGTTCCGA	AGGGAAGTTT	CTTCGGCATT	ATTGGACCAA	ATGGTTCGGG	3420
AAAAACCACG	CTACTCTCAC	TCATTATGAA	ATTCCAAAAG	CCAAAAAGTG	GGAAAAATAAC	3480
AGTTGATGGG	AACGATGTGC	TCAGGCTATC	TCACAAAAAA	CTTGCACAAC	TTATAGCATA	3540
CATCGCTCAA	GACTTTAACC	CTACATACGA	TTTCACAGTT	GAAGAATTGG	TCGAAATGGG	3600
AGGAATCCCC	CGCTCACCAC	ATTTTTTCGA	AACACCTGTT	TACGAGGAAG	AATTAGAAAA	3660
TGCACTCAAA	ACTGTTGATT	TGCTTGAATA	CCGAAAAAGA	ATATTCTCCA	CTCTTAGTGG	3720
AGGACAACAG	CGCAGGGTCT	TGATTGCACG	CGCAATCTAT	CAAAACACAC	CTATCATCAT	3780
TGCTGATGAA	TTGGTTAATC	ACTTGGATTT	AGGCCAAGCA	ATTAAGTGT	TAGATTATCT	3840
AAACAACCTT	ACCGAATGTG	GAAAGACGAT	AATTGGACAT	TCCACCTGCA	GCCCGG	3896

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGTGCTGCA	AGGCGATTAA	GTGGAACG	CCAGGTTTTC	CCAGTCACGA	CGTTGTAAAA	60
CGACGGCCAG	TGAATTGTAA	TACGACTCAC	TATAGGGCGA	ATTGGGTACC	GGGCCCCCCC	120
TCGAGGTCGA	CGGTATCGAT	AAGCTTGATA	TCGAATTCG	TACGAAATGC	GGGAAAGAGA	180
GAAGGAAAAG	GAAAGAGAGC	ACAGATTTGG	AAATGAGACA	GAACACGAGG	AAGAGCATGG	240
TATGGCAGAG	CGTGAAAGAG	CACATGAGAA	CGAGTCTGAA	GAAATGGGCA	AGGGCGTTGG	300
CATGGGCGCC	CATGGAATGA	AGATGGGCAA	AGAAGCTCGC	GAAATGGTGA	AGGAAGAATA	360
CAAGGAAGCA	AAGGAGAGAT	ACAAGAAGGC	TAGAGAAGAG	TTTGAAAGAG	CAAAGAAGAT	420
GGGATTGGAC	ATCAGAGAGG	AGCGCGGATT	CAAGATGGCC	AAGGGATTCA	TGGTAGCTGG	480
ACTAGACGTT	GCTGAGATGT	GGCTGGAGAG	ACTGAAGGTA	CAGGTCATGA	ATATGGGTGA	540
AGAGGCCAAG	ATCAGAGAGG	AGACCAAAT	GGAGCTGCTC	GCAAAGATCG	ACGAGAAGCT	600
TGCAGAAATC	AAAGAGCTGA	AGAACGAAAT	CAATGAGACC	TCCTCACCTG	AAGAGCTGAT	660
AGAAACTGTC	AAGAAAATCA	GAAAGGAGTG	GAGAGAAATC	AGAGATGAAA	TGAGGGCTCT	720
TACTGGCTAT	GTCGCCGTTG	CCAAGGTGGA	AAAGCTTGTT	GAAAAGGCCA	AGCAGGTAGA	780
GCTAATGCTT	GAGGCAAGA	TCGAGGAGCT	CGATGCTGCA	GGAGTTGATA	CAACCAAAT	840
CGAGGCAACA	CTCGAGGACT	TCTCGGCAAA	GGTTAATGAA	GCAGAAGATT	TGATTGACAA	900
GGCTGAAAAT	CTGTTTCGAGG	AAGGCAACAT	TGCTGAAGGA	CACATGACTC	TCAAGGAAGC	960
CATAAAGACT	CTCAAGGAAG	CCTTCAAGGA	TGTCAAGGAA	GTTGTCAGCG	AGATGAAGGA	1020
AATGAACCAG	TATAGAGTTA	GGGAGGGCAA	GATCTTCTAC	GGAAACGAGA	CTGGAGAAGT	1080
CTGGGTGGAT	GGTAATGGTA	CTGCTGAGTT	TAACGGTACC	GGTATCGTTG	TGATCAGAGG	1140
AAACGCAACA	CTTGAGGTCTG	CACCAGAAGA	TGCGATCGTG	AACTGGTCTG	GCTTCGGCGT	1200
GAAGAGCGTT	GAGGGTGGCG	TTTCAAGAGT	CAGCGGAGAA	GGTAAGGCAG	TAATCAGAGG	1260
AGAAAACCTC	ACCGTCAAGG	TGGAAGGTGA	CGACTTCAAG	CTCATAGTGA	AGGGCTACGG	1320
TACACTCAAA	CTCGATGGTG	AGGGTGAATA	CAGGGTAAAG	AAGAGCCAC	AGGAAGAGAT	1380
GACATTTAAA	CTCTTTCTTC	AACTCTAGCA	GTTTGAGCAT	TGCATTTCCA	AGATTTTTCG	1440
TGTTAGCTTC	GGGACAACCT	TGAAAATACG	TCGAGACAGG	CTCAAATGTT	GTCCAGCAT	1500
TGCAGCTTTC	GGCAAAGCGA	ACGAGATTTG	CGTTCGCTC	CCCAGCCCAA	CATGGCTTCT	1560

GTAATCTGAA	AAAAC TTCAA	GTTCAACAGC	TTTCCCAAAA	ACATCCAAAA	GCTTTTCCGC	1620
AACACTTCTA	AATCTTTTCA	GATTTTATTG	ATTTCTTTTC	ACCGAAATGC	TATCGGATTC	1680
TCTTCCCACA	ACCTCGATAT	GCGGCTCTTC	CAGAGCAATA	CCCACTCCAC	CGTCAATCCT	1740
TCCAACCTGG	CCGTTCAAAT	CAATGAGCGT	GATATGAATT	CTCGACGGAG	TTTTAACCTT	1800
AACATACATC	TATAGAAATT	AAACGGTAAT	TACTTAAGAA	GTTTTGGTTT	TGCGAAAAAG	1860
AGTTCAAAAT	TCATTCTTTT	AACTGCACTA	CAGCTCATCT	GTGCCTTTTC	TCCTTAATTC	1920
GATTTTCTG	AGATAGTTCT	GGTATCTCGT	ATCAACTATG	TAAGCCTCGG	GAGCTATTAC	1980
AGGCAGATGA	TAACCGGTGA	ATATCCTTAT	TATCTCTCCA	GCCTGAACCG	AGCATGTCAG	2040
TGCATATGAT	ATCGGATCGT	GATCGATGTG	AGGATACTCC	ACCTCGAAGA	AAGACACACC	2100
ATCAGGCAGG	AAAGTAGTAA	TTATATCGGG	AATAAATGGA	GCTCCGAGCT	CTTCAGCAAC	2160
TTTTGACAGC	ATTGAAATGT	GCTTATGAGC	AACAACAACA	TCAATACCTT	TCAACTGTCT	2220
CCTGAGTTCT	TTATAATCAT	GCGGGAAGGG	ATAAGAGATT	ATACACGAAT	CAGAACTCAT	2280
AGGATGCACA	ACATCATAAT	CGTTTGCCCTC	AAGTGGCTTT	ATGCTGGCAT	CAAGCCTCAC	2340
ATCCATTGGT	GTAAC TACAT	CTCCAATATA	CCGAATGCAA	CCAACACCAC	TTCTCCAGAG	2400
CAATTCCATG	AGCATTCTGC	TTCCGATGAC	AGCGACACTA	AAGTTCTCTGA	GATAATCTAT	2460
CTTTTCTTCA	TCTGCCATCC	CATACCAGGA	AATTTTCTCT	ATGGCAATAG	CCCCGCATCC	2520
ATTAAATGGT	ATTAATTTT	TGCCGTATTT	TGAGGAGGTA	GATATTAACC	AATTATTTTC	2580
AAACCATTTA	AGGGCATCGA	TGAAACATCC	CAAAACCAGT	TCAGCAAAAA	ATTAAATCAC	2640
TGCCACACAT	TGAGGACCCC	AAAATGGTGT	GAGAAATGGA	CGAACTGGGA	GGAGTTATTT	2700
TTGATCTGAT	AGAAGAGGAG	CCCGAAGTTG	AGGAGGACGA	CGAGATTAAG	CTCGCAGAGA	2760
TATACAGGCT	TGCTACAAAA	CTTATAAAGT	TACTCGAAGA	TCTCAAAAGC	CATGAGCTTA	2820
AAGAGTCAGC	ATCTCTTATG	CTCATAAAGG	AAATTATCGG	TGAAGACAGA	GTTCTGGTTG	2880
GTTTAGCATC	AAAAATGCTC	CAGGATATGA	GTCTCGGGTT	CGAAGAGGAC	GAAAAGTACG	2940
TTTCTTGATT	TTTGAAC TGT	ATTTTCTACA	TGCTCTTTTC	CCAACCACAT	TCAGTTGCAT	3000
GCCATACGAA	AATTCCAATG	CCCAAATCCT	GGTAAATGTA	CTTTTTCATA	GTAAATGCTG	3060
CCAAACCCAG	ATTAAACTCA	ATTTTCATCAA	CAGGAAAAAG	AAAGAACGAA	AAAAAGACCT	3120
ACAACAGTCC	TATAATTGAC	CAAAC TTGAT	AGATTACAAA	CACCACAGTT	GGAATCAAAG	3180
CACAGATGAA	AGCTTTCGG	ATTCCTGCAG	CC			3212

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG GAA ATA ATA AAC AAA TTT CTA AAA AAA ATT GGA TAT AAG AAA GAT	48
Met Glu Ile Ile Asn Lys Phe Leu Lys Lys Ile Gly Tyr Lys Lys Asp	
1 5 10 15	
GGA GAA GAA AAA AAG GAC AAA TCT AAA ACC AAA ATA AAA ATT GAA GAA	96
Gly Glu Glu Lys Lys Asp Lys Ser Lys Thr Lys Ile Lys Ile Glu Glu	
20 25 30	
GAA AAA ACC ATG GAT ATC GAA ATT CCA AAA ATT GAA CCT ACT GAA AAT	144
Glu Lys Thr Met Asp Ile Glu Ile Pro Lys Ile Glu Pro Thr Glu Asn	
35 40 45	
TTT AAT CGT GAT GAA ATT GTT TTT GAG GAA GAT AAT GCC TAC GGT ATA	192
Phe Asn Arg Asp Glu Ile Val Phe Glu Glu Asp Asn Ala Tyr Gly Ile	
50 55 60	
TCC CAC AAA GGA AAT AGA ACA AAC AAC GAA GAC AAT ATT TTA ATT AGA	240
Ser His Lys Gly Asn Arg Thr Asn Asn Glu Asp Asn Ile Leu Ile Arg	
65 70 75 80	

AAA ATA AAA GAT ACC TAC ATA TTA GCA GTT GCA GAT GGT GTC GGA GGG Lys Ile Lys Asp Thr Tyr Ile Leu Ala Val Ala Asp Gly Val Gly Gly 85 90 95	288
CAC AGC TCA GGA GAT GTT GCA TCA AAG ATG GCA GTG GAT ATT TTA GAA His Ser Ser Gly Asp Val Ala Ser Lys Met Ala Val Asp Ile Leu Glu 100 105 110	336
AAC ATT ATC ATG GAA AAA TAC AAT GAA AAC CTA TCA ATT GAA GAG ATA Asn Ile Ile Met Glu Lys Tyr Asn Glu Asn Leu Ser Ile Glu Glu Ile 115 120 125	384
AAA GAA CTT TTA AAA GAT GCA TAC ATT ACG GCA CAC AAC AAA ATA AAA Lys Glu Leu Leu Lys Asp Ala Tyr Ile Thr Ala His Asn Lys Ile Lys 130 135 140	432
GAA AAC GCT ATT GGA GAT AAA GAG GGA ATG GGA ACA ACA CTA ACA ACT Glu Asn Ala Ile Gly Asp Lys Glu Gly Met Gly Thr Thr Leu Thr Thr 145 150 155 160	480
GCA ATA GTT AAA GGG GAT AAA TGC GTT ATA GCA AAC TGC GGG GAT AGT Ala Ile Val Lys Gly Asp Lys Cys Val Ile Ala Asn Cys Gly Asp Ser 165 170 175	528
AGG GCT TAT TTA ATT AGA GAT GGA GAA ATA GTT TTT AGA ACA AAA GAC Arg Ala Tyr Leu Ile Arg Asp Gly Glu Ile Val Phe Arg Thr Lys Asp 180 185 190	576
CAC TCT TTG GTT CAG GTT TTA GTA GAT GAA GGA CAT ATT TCA GAG GAG His Ser Leu Val Gln Val Leu Val Asp Glu Gly His Ile Ser Glu Glu 195 200 205	624
GAC GCA AGG CAT CAT CCA ATG AAA AAT ATC ATT ACC TCA GCA TTG GGA Asp Ala Arg His His Pro Met Lys Asn Ile Ile Thr Ser Ala Leu Gly 210 215 220	672
TTG GAT GAA TTT AAG GTA GAT GAT TAC GAA TGG GAT TTA ATT GAT GGT Leu Asp Glu Phe Lys Val Asp Asp Tyr Glu Trp Asp Leu Ile Asp Gly 225 230 235 240	720
GAT GTA TTA TTG ATG AGC TCC GAT GGG CTT CAT GAT TAT GTC AGT AAG Asp Val Leu Leu Met Ser Ser Asp Gly Leu His Asp Tyr Val Ser Lys 245 250 255	768
GAA GAT ATT TTA AAA ACT GTA AAA AAT AAT GAT CAC CCA AAA GAT ATT Glu Asp Ile Leu Lys Thr Val Lys Asn Asn Asp His Pro Lys Asp Ile 260 265 270	816
GTA GAT GAA TTA TTC AAT ACT GCA TTA AAA GAG ACA AGG GAC AAT GTG Val Asp Glu Leu Phe Asn Thr Ala Leu Lys Glu Thr Arg Asp Asn Val 275 280 285	864
AGT ATT ATT CGT ATA Ser Ile Ile Arg Ile 290	879

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Glu	Ile	Ile	Asn	Lys	Phe	Leu	Lys	Lys	Ile	Gly	Tyr	Lys	Lys	Asp	
1				5				10						15		
Gly	Glu	Glu	Lys	Lys	Asp	Lys	Ser	Lys	Thr	Lys	Ile	Lys	Ile	Glu	Glu	
			20					25					30			
Glu	Lys	Thr	Met	Asp	Ile	Glu	Ile	Pro	Lys	Ile	Glu	Pro	Thr	Glu	Asn	
			35				40					45				
Phe	Asn	Arg	Asp	Glu	Ile	Val	Phe	Glu	Glu	Asp	Asn	Ala	Tyr	Gly	Ile	
	50				55					60						
Ser	His	Lys	Gly	Asn	Arg	Thr	Asn	Asn	Glu	Asp	Asn	Ile	Leu	Ile	Arg	
	65			70				75					80			
Lys	Ile	Lys	Asp	Thr	Tyr	Ile	Leu	Ala	Val	Ala	Asp	Gly	Val	Gly	Gly	
			85					90					95			
His	Ser	Ser	Gly	Asp	Val	Ala	Ser	Lys	Met	Ala	Val	Asp	Ile	Leu	Glu	
			100					105				110				
Asn	Ile	Ile	Met	Glu	Lys	Tyr	Asn	Glu	Asn	Leu	Ser	Ile	Glu	Glu	Ile	
	115						120					125				
Lys	Glu	Leu	Leu	Lys	Asp	Ala	Tyr	Ile	Thr	Ala	His	Asn	Lys	Ile	Lys	
	130					135					140					
Glu	Asn	Ala	Ile	Gly	Asp	Lys	Glu	Gly	Met	Gly	Thr	Thr	Leu	Thr	Thr	
	145			150				155					160			
Ala	Ile	Val	Lys	Gly	Asp	Lys	Cys	Val	Ile	Ala	Asn	Cys	Gly	Asp	Ser	
			165					170				175				
Arg	Ala	Tyr	Leu	Ile	Arg	Asp	Gly	Glu	Ile	Val	Phe	Arg	Thr	Lys	Asp	
			180				185					190				
His	Ser	Leu	Val	Gln	Val	Leu	Val	Asp	Glu	Gly	His	Ile	Ser	Glu	Glu	
	195					200					205					
Asp	Ala	Arg	His	His	Pro	Met	Lys	Asn	Ile	Ile	Thr	Ser	Ala	Leu	Gly	
	210					215					220					
Leu	Asp	Glu	Phe	Lys	Val	Asp	Asp	Tyr	Glu	Trp	Asp	Leu	Ile	Asp	Gly	
	225				230				235				240			
Asp	Val	Leu	Leu	Met	Ser	Ser	Asp	Gly	Leu	His	Asp	Tyr	Val	Ser	Lys	
			245					250				255				
Glu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Asn	Asn	Asp	His	Pro	Lys	Asp	Ile	
			260					265				270				
Val	Asp	Glu	Leu	Phe	Asn	Thr	Ala	Leu	Lys	Glu	Thr	Arg	Asp	Asn	Val	
	275					280						285				
Ser	Ile	Ile	Arg	Ile												
	290															

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG	ACT	CTG	CTA	GCC	CTG	TAT	CAG	AAT	AAA	CGT	GTT	ATC	GTC	AAG	CTT	
Met	Thr	Leu	Leu	Ala	Leu	Tyr	Gln	Asn	Lys	Arg	Val	Ile	Val	Lys	Leu	
1				5				10						15		
GGC	TGG	GGG	AGC	GGC	ACT	AGC	CAA	ATA	ACT	AAC	GAG	GCG	CAA	GTG	CTG	
Gly	Trp	Gly	Ser	Gly	Thr	Ser	Gln	Ile	Thr	Asn	Glu	Ala	Gln	Val	Leu	

48

96

			20				25				30							
AGC Ser	GTA Val	TTG Leu 35	CAC His	GAT Asp	ATG Met	CCT Pro	ATA Ile 40	GTG Val	CCC Pro	AGA Arg	CTG Leu	CAT His 45	ACC Thr	CGT Arg	CTA Leu	144		
GAC Asp	TTA Leu 50	GAT Asp	GAT Asp	GTC Val	AAG Lys	CTC Leu 55	GTT Val	GCG Ala	ATA Ile	GAG Glu	TAC Tyr 60	ATA Ile	CCC Pro	TAC Tyr	AAG Lys	192		
AGC Ser 65	CTT Leu	AAC Asn	GCC Ala	GTC Val	GGC Gly 70	CGC Arg	TTG Leu	AAC Asn	CCC Pro	CTT Leu 75	AAG Lys	GCT Ala	GTC Val	ACA Thr	GCC Ala 80	240		
GTC Val	TTC Phe	TAT Tyr	ACA Thr 85	CTC Leu	GCA Ala	TCG Ser	CTA Leu	GTC Val	CAT His 90	ATC Ile	CAC His	GGC Gly	CGT Arg	GGT Gly 95	TTT Phe	288		
GCT Ala	CAT His	TGC Cys	GAC Asp 100	CTA Leu	AAG Lys	CCG Pro	GGT Gly	AAC Asn 105	GTT Val	ATA Ile	CCA Pro	GTT Val	CCC Pro 110	AAG Lys	CGT Arg	336		
GGC Gly	ATG Met 115	GTG Val	TTC Phe	ATC Ile	GAC Asp	TTT Phe	GGT Gly 120	GTT Val	GCA Ala	CGA Arg	CCT Pro	TTT Phe 125	GAC Asp	GCT Ala	GCG Ala	384		
GGC Gly 130	TTC Phe	GCG Ala	GCA Ala	GGA Gly	ACA Thr	CCA Pro 135	GGG Gly	TAT Tyr	ACG Thr	TGC Cys	CCA Pro 140	GAG Glu	GCT Ala	CTC Leu	GGC Gly	432		
GGC Gly 145	GAG Glu	ACC Thr	CCC Pro	GGC Gly	TCT Ser 150	GGC Gly	TGC Cys	GAT Asp	CTC Leu	TAC Tyr 155	AGC Ser	CTT Leu	GCC Ala	GGC Gly	ATA Ile 160	480		
TAC Tyr	TAC Tyr	TAC Tyr	TTG Leu 165	GTT Val	ACC Thr	GGG Gly	TTA Leu	AGC Ser	CCG Pro 170	CCA Pro	CGC Arg	GAC Asp	CCA Pro	AAA Lys 175	GAG Glu	528		
TTC Phe	GCC Ala	AAG Lys	GCG Ala 180	CTC Leu	TCG Ser	TTG Leu	GCT Ala	CCC Pro 185	GCT Ala	CCA Pro	AGT Ser	AGC Ser	CTC Leu 190	TTG Leu	GAA Glu	576		
CTG Leu	TTC Phe	ACA Thr 195	CAG Gln	CTG Leu	GTG Val	CTG Leu	GAT Asp 200	CCC Pro	GAG Glu	TAT Tyr	CGT Arg	AAC Asn 205	AGC Ser	CTT Leu	GAT Asp	624		
CCT Pro	CTC Leu 210	CAG Gln	CTG Leu	TTG Leu	AAG Lys	ATT Ile 215	GTT Val	GCA Ala	TCT Ser	TTT Phe	AAC Asn 220	CCG Pro	CAA Gln	CTG Leu	CTA Leu	672		
GTC Val 225	CCT Pro	CAT His	ATC Ile	GTT Val	ATA Ile 230	GAT Asp	GGT Gly	GTT Val	TAC Tyr	AAG Lys 235	CCG Pro	CTA Leu	GGT Gly	TAC Tyr	GGC Gly 240	720		
GAG Glu	GTA Val	AGC Ser	ATA Ile 245	GGC Gly	TCT Ser	AGA Arg	GGC Gly	GTT Val	ATA Ile 250	CGT Arg	GTT Val	GAT Asp	GGA Gly	CGA Arg 255	CCA Pro	768		
GTG Val	TAC Tyr	CTC Leu	GCG Ala 260	GTT Val	AAG Lys	AGG Arg	CAT His	GTG Val 265	AGG Arg	GGC Gly	ACA Thr	AGT Ser	ATG Met 270	TAC Tyr	GCG Ala	816		
TAT Tyr	ACG Thr	GAT Asp 275	CTT Leu	GTC Val	GTG Val	TTT Phe	AGG Arg 280	AGA Arg	GGC Gly	GAG Glu	AAA Lys 285	CTC Leu	ATA Ile	GTG Val	AGA Arg	864		

AGC GGT GAG AGT ATA GAC CTA GAG TTT AAC GAC CTG GTG TTG TTC GAC 912
 Ser Gly Glu Ser Ile Asp Leu Glu Phe Asn Asp Leu Val Leu Phe Asp
 290 295 300

AAC CAC ATA CTA TAC GTA TTT ATC CTT CCG GAA AGG CCC 951
 Asn His Ile Leu Tyr Val Phe Ile Leu Pro Glu Arg Pro
 305 310 315

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Thr Leu Leu Ala Leu Tyr Gln Asn Lys Arg Val Ile Val Lys Leu
 1 5 10 15
 Gly Trp Gly Ser Gly Thr Ser Gln Ile Thr Asn Glu Ala Gln Val Leu
 20 25 30
 Ser Val Leu His Asp Met Pro Ile Val Pro Arg Leu His Thr Arg Leu
 35 40 45
 Asp Leu Asp Asp Val Lys Leu Val Ala Ile Glu Tyr Ile Pro Tyr Lys
 50 55 60
 Ser Leu Asn Ala Val Gly Arg Leu Asn Pro Leu Lys Ala Val Thr Ala
 65 70 75 80
 Val Phe Tyr Thr Leu Ala Ser Leu Val His Ile His Gly Arg Gly Phe
 85 90 95
 Ala His Cys Asp Leu Lys Pro Gly Asn Val Ile Pro Val Pro Lys Arg
 100 105 110
 Gly Met Val Phe Ile Asp Phe Gly Val Ala Arg Pro Phe Asp Ala Ala
 115 120 125
 Gly Phe Ala Ala Gly Thr Pro Gly Tyr Thr Cys Pro Glu Ala Leu Gly
 130 135 140
 Gly Glu Thr Pro Gly Ser Gly Cys Asp Leu Tyr Ser Leu Ala Gly Ile
 145 150 155 160
 Tyr Tyr Tyr Leu Val Thr Gly Leu Ser Pro Pro Arg Asp Pro Lys Glu
 165 170 175
 Phe Ala Lys Ala Leu Ser Leu Ala Pro Ala Pro Ser Ser Leu Leu Glu
 180 185 190
 Leu Phe Thr Gln Leu Val Leu Asp Pro Glu Tyr Arg Asn Ser Leu Asp
 195 200 205
 Pro Leu Gln Leu Leu Lys Ile Val Ala Ser Phe Asn Pro Gln Leu Leu
 210 215 220
 Val Pro His Ile Val Ile Asp Gly Val Tyr Lys Pro Leu Gly Tyr Gly
 225 230 235 240
 Glu Val Ser Ile Gly Ser Arg Gly Val Ile Arg Val Asp Gly Arg Pro
 245 250 255
 Val Tyr Leu Ala Val Lys Arg His Val Arg Gly Thr Ser Met Tyr Ala
 260 265 270
 Tyr Thr Asp Leu Val Val Phe Arg Arg Gly Glu Lys Leu Ile Val Arg
 275 280 285
 Ser Gly Glu Ser Ile Asp Leu Glu Phe Asn Asp Leu Val Leu Phe Asp
 290 295 300
 Asn His Ile Leu Tyr Val Phe Ile Leu Pro Glu Arg Pro
 305 310 315

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATG GAC ATC AGG GCC GTT GTT TTT GAC CTC GAC GGG ACG CTT GTG GGT	48
Met Asp Ile Arg Ala Val Val Phe Asp Leu Asp Gly Thr Leu Val Gly	
1 5 10 15	
GCT GAG AAG ACT TTC AGC GAG ATA AAG TCC GAG CTT AAA GAA CGG CTG	96
Ala Glu Lys Thr Phe Ser Glu Ile Lys Ser Glu Leu Lys Glu Arg Leu	
20 25 30	
ATT TCC TTA GGG ATT CCC AGG GAG CTC GTT GGA GAG CTA ACG CCG ATG	144
Ile Ser Leu Gly Ile Pro Arg Glu Leu Val Gly Glu Leu Thr Pro Met	
35 40 45	
TAT GAG GGC CTT ATC GAG CTG TCC AGA AAA ACG GGC AGA CCT TTC GAA	192
Tyr Glu Gly Leu Ile Glu Leu Ser Arg Lys Thr Gly Arg Pro Phe Glu	
50 55 60	
GAG ATG TAC TCA ATT CTC GTC AAT CTT GAA GTT GAA AGG ATA AGG GAC	240
Glu Met Tyr Ser Ile Leu Val Asn Leu Glu Val Glu Arg Ile Arg Asp	
65 70 75 80	
AGC TTT CTC TTC GAG GGG GCA AGG GAG CTC CTC GAC TTT CTT GTG GGG	288
Ser Phe Leu Phe Glu Gly Ala Arg Glu Leu Leu Asp Phe Leu Val Gly	
85 90 95	
GAG GGA ATA AAG CTT GCC CTC ATG ACC CGG AGC TCC AGA ATG GCT GCC	336
Glu Gly Ile Lys Leu Ala Leu Met Thr Arg Ser Ser Arg Met Ala Ala	
100 105 110	
CTT GAG GCC CTG GAG CTT CAC GGC ATT AAG GAC TAC TTT GAG ATT ATT	384
Leu Glu Ala Leu Glu Leu His Gly Ile Lys Asp Tyr Phe Glu Ile Ile	
115 120 125	
TCA ACG AGG GAT GAT GTC CCT CCC GAG GAG CTG AAA CCG AAT CCT GGC	432
Ser Thr Arg Asp Asp Val Pro Pro Glu Glu Leu Lys Pro Asn Pro Gly	
130 135 140	
CAG CTG AGG AGA ATC CTC GGT GAG CTC AAC GTT CAA CCA GAG AAA GCC	480
Gln Leu Arg Arg Ile Leu Gly Glu Leu Asn Val Gln Pro Glu Lys Ala	
145 150 155 160	
ATC GTC GTT GGA GAC CAC GGC TAC GAT GTC ATC CCT GCC CGG GAG CTC	528
Ile Val Val Gly Asp His Gly Tyr Asp Val Ile Pro Ala Arg Glu Leu	
165 170 175	
GGC GCT CTG AGC GTC CTT GTC ACC GGC CAC GAG GCT GGC AGA ATG AGC	576
Gly Ala Leu Ser Val Leu Val Thr Gly His Glu Ala Gly Arg Met Ser	
180 185 190	
TTT CAG GTT GAA GCC GAG CCA AAC TTT GAG GTC GAG AAC CTC ATT CAC	624
Phe Gln Val Glu Ala Glu Pro Asn Phe Glu Val Glu Asn Leu Ile His	
195 200 205	

CTC AGG AAG CTC TTC GAG AGG CTC CTG TCG AGC TAC GTT GTT GTT CCC Leu Arg Lys Leu Phe Glu Arg Leu Leu Ser Ser Tyr Val Val Val Pro 210 215 220	672
GCT TAC AAC GAG GAG AAG ACC ATC AAG GGG GTA ATA GAG AAT CTT CTC Ala Tyr Asn Glu Glu Lys Thr Ile Lys Gly Val Ile Glu Asn Leu Leu 225 230 235 240	720
AGG TAT TTC AAA AAG GAC GAG ATA ATC GTC GTG AAC GAC GGC TCC AGG Arg Tyr Phe Lys Lys Asp Glu Ile Ile Val Val Asn Asp Gly Ser Arg 245 250 255	768
GAT AGA ACG GAG GAG ATA GCT CGT TCT TAC GGA GTC CAC GTT CTT ACG Asp Arg Thr Glu Glu Ile Ala Arg Tyr Gly Val His Val Leu Thr 260 265 270	816
CAT CTC GTC AAC AGG GGG CTT GGT GGG GCC CTC GGA ACG GGC TTT GCC His Leu Val Asn Arg Gly Leu Gly Gly Ala Leu Gly Thr Gly Phe Ala 275 280 285	864
TAT GCC ATC AGA AAA AAC GCC AAA CTT GTC CTC ACA TTT GAT GCC GAC Tyr Ala Ile Arg Lys Asn Ala Lys Leu Val Leu Thr Phe Asp Ala Asp 290 295 300	912
GGC CAG CAC CTT ATA AGC GAC GCC CTC CGC GTC ATG AGG CCA GTT GCG Gly Gln His Leu Ile Ser Asp Ala Leu Arg Val Met Arg Pro Val Ala 305 310 315 320	960
GAG GGC AGG GCG GAC TTT GCG GTC GGC TCA AGG CTC AAA GGT GAC ACG Glu Gly Arg Ala Asp Phe Ala Val Gly Ser Arg Leu Lys Gly Asp Thr 325 330 335	1008
AGC CAG ATG CCC CTC GTG AAG AAG TTC GGC AAC TTC GTT CTA GAT GCC Ser Gln Met Pro Leu Val Lys Lys Phe Gly Asn Phe Val Leu Asp Ala 340 345 350	1056
GTG ACC GCG GTT TTT GCT GGT AAA TAC GTC AGC GAC AGT CAG AGC GGG Val Thr Ala Val Phe Ala Gly Lys Tyr Val Ser Asp Ser Gln Ser Gly 355 360 365	1104
TTA AGG TGT CTA AGC GGC GAC TGC CTG AGG AAA ATC AGG ATA ACC TGC Leu Arg Cys Leu Ser Gly Asp Cys Leu Arg Lys Ile Arg Ile Thr Cys 370 375 380	1152
GAC CGC TAT GCC GTG TCG AGT GAG ATT ATA ATA GAG GCC TCC AAA GCG Asp Arg Tyr Ala Val Ser Ser Glu Ile Ile Ile Glu Ala Ser Lys Ala 385 390 395 400	1200
GGC TGT AGA ATT GTC GAA GTT CCT ATC AAG GCT GTT TAC ACT GAG TAC Gly Cys Arg Ile Val Glu Val Pro Ile Lys Ala Val Tyr Thr Glu Tyr 405 410 415	1248
TTT ATG AAG AAG GGG ACG AAC GTT TTA GAG GGC GTT AAG ATA GCC CTG Phe Met Lys Lys Gly Thr Asn Val Leu Glu Gly Val Lys Ile Ala Leu 420 425 430	1296
AAC CTT CTC TTT GAC AAA CTG AGG Asn Leu Leu Phe Asp Lys Leu Arg 435 440	1320

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met 1	Asp	Ile	Arg	Ala 5	Val	Val	Phe	Asp	Leu 10	Asp	Gly	Thr	Leu	Val 15	Gly
Ala	Glu	Lys	Thr	Phe 20	Ser	Glu	Ile	Lys 25	Ser	Glu	Leu	Lys	Glu	Arg	Leu
Ile	Ser	Leu 35	Gly	Ile	Pro	Arg	Glu 40	Leu	Val	Gly	Glu	Leu 45	Thr	Pro	Met
Tyr	Glu 50	Gly	Leu	Ile	Glu 55	Leu	Ser	Arg	Lys	Thr	Gly 60	Arg	Pro	Phe	Glu
Glu 65	Met	Tyr	Ser	Ile 70	Val	Asn	Leu	Glu 75	Val	Glu	Arg	Ile	Arg	Asp 80	
Ser	Phe	Leu	Phe 85	Glu	Gly	Ala	Arg	Glu 90	Leu	Leu	Asp	Phe	Leu 95	Val	Gly
Glu	Gly	Ile 100	Lys	Leu	Ala	Leu	Met 105	Thr	Arg	Ser	Ser	Arg	Met 110	Ala	Ala
Leu	Glu 115	Ala	Leu	Glu	Leu	His	Gly 120	Ile	Lys	Asp	Tyr	Phe 125	Glu	Ile	Ile
Ser	Thr 130	Arg	Asp	Asp	Val	Pro	Pro 135	Glu	Glu	Leu	Lys 140	Pro	Asn	Pro	Gly
Gln 145	Leu	Arg	Arg	Ile 150	Leu	Gly	Glu	Leu	Asn 155	Val	Gln	Pro	Glu	Lys	Ala 160
Ile	Val	Val	Gly 165	Asp	His	Gly	Tyr	Asp 170	Val	Ile	Pro	Ala	Arg	Glu 175	Leu
Gly	Ala 180	Leu	Ser	Val	Leu	Val	Thr 185	Gly	His	Glu	Ala	Gly 190	Arg	Met	Ser
Phe	Gln 195	Val	Glu	Ala	Glu	Pro	Asn 200	Phe	Glu	Val	Glu	Asn 205	Leu	Ile	His
Leu	Arg 210	Lys	Leu	Phe	Glu 215	Arg	Leu	Leu	Ser	Ser	Tyr 220	Val	Val	Val	Pro
Ala 225	Tyr	Asn	Glu	Glu 230	Lys	Thr	Ile	Lys	Gly 235	Val	Ile	Glu	Asn	Leu 240	Leu
Arg	Tyr	Phe	Lys 245	Lys	Asp	Glu	Ile	Ile	Val 250	Val	Asn	Asp	Gly 255	Ser	Arg
Asp	Arg	Thr 260	Glu	Glu	Ile	Ala	Arg 265	Ser	Tyr	Gly	Val	His 270	Val	Leu	Thr
His	Leu 275	Val	Asn	Arg	Gly	Leu	Gly 280	Gly	Ala	Leu	Gly	Thr 285	Gly	Phe	Ala
Tyr	Ala 290	Ile	Arg	Lys	Asn 295	Ala	Lys	Leu	Val	Leu	Thr 300	Phe	Asp	Ala	Asp
Gly 305	Gln	His	Leu	Ile 310	Ser	Asp	Ala	Leu	Arg 315	Val	Met	Arg	Pro	Val	Ala 320
Glu	Gly	Arg	Ala 325	Asp	Phe	Ala	Val	Gly 330	Ser	Arg	Leu	Lys	Gly 335	Asp	Thr
Ser	Gln 340	Met	Pro	Leu	Val	Lys	Lys 345	Phe	Gly	Asn	Phe	Val 350	Leu	Asp	Ala
Val	Thr 355	Ala	Val	Phe	Ala	Gly 360	Lys	Tyr	Val	Ser	Asp 365	Ser	Gln	Ser	Gly
Leu	Arg 370	Cys	Leu	Ser	Gly 375	Asp	Cys	Leu	Arg	Lys	Ile 380	Arg	Ile	Thr	Cys
Asp 385	Arg	Tyr	Ala	Val 390	Ser	Ser	Glu	Ile	Ile 395	Ile	Glu	Ala	Ser	Lys	Ala 400
Gly	Cys	Arg	Ile 405	Val	Glu	Val	Pro	Ile 410	Lys	Ala	Val	Tyr	Thr 415	Glu	Tyr
Phe	Met 420	Lys	Lys	Gly	Thr	Asn	Val 425	Leu	Glu	Gly	Val	Lys 430	Ile	Ala	Leu
Asn	Leu 435	Leu	Phe	Asp	Lys	Leu	Arg 440								

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATG GAA AAT CTT GAA AAA CTC CTT GAA GTG GCA AAG ATG GCA GCC CTT	48
Met Glu Asn Leu Glu Lys Leu Leu Glu Val Ala Lys Met Ala Ala Leu	
1 5 10 15	
GCC GGA GGA CAG GTA TTA AAG GAA AAC TTC GGA AAG ATT AAG CTT GAA	96
Ala Gly Gly Gln Val Leu Lys Glu Asn Phe Gly Lys Ile Lys Leu Glu	
20 25 30	
AAC ATT GAA GAA AAG GGA GAG AAG GAC TTC GTG AGC TAC GTT GAT AAA	144
Asn Ile Glu Glu Lys Gly Glu Lys Asp Phe Val Ser Tyr Val Asp Lys	
35 40 45	
ACC TCC GAA GAG AGA ATA AAA GAG CTA ATA CTT AAG TTC TTT CCC GAC	192
Thr Ser Glu Glu Arg Ile Lys Glu Leu Ile Leu Lys Phe Phe Pro Asp	
50 55 60	
CAC GAG GTC GTG GGG GAG GAA AGG GGA AAG GAG GGA AAA GAA AGC CCT	240
His Glu Val Val Gly Glu Glu Arg Gly Lys Glu Gly Lys Glu Ser Pro	
65 70 75 80	
TAC AAA TGG TTC ATA GAC CCC CTT GAT GGG ACC AAG AAC TAC ATA AAG	288
Tyr Lys Trp Phe Ile Asp Pro Leu Asp Gly Thr Lys Asn Tyr Ile Lys	
85 90 95	
GGC TTT CCC ATA TTT GCA GTC TCC GTC GGA CTC GTT AAG GAA AAC GAA	336
Gly Phe Pro Ile Phe Ala Val Ser Val Gly Leu Val Lys Glu Asn Glu	
100 105 110	
CCT ATA GTG GGA GCG GTT TAC CTT CCT TAC TTT GAT ACC CTA TAC TGG	384
Pro Ile Val Gly Ala Val Tyr Leu Pro Tyr Phe Asp Thr Leu Tyr Trp	
115 120 125	
GCT TCA AAG GGA AGG GGA GCC TAT AAA AAC GGG GAG AGG ATA AGC GTA	432
Ala Ser Lys Gly Arg Gly Ala Tyr Lys Asn Gly Glu Arg Ile Ser Val	
130 135 140	
AAG GAA AGG GGG GAG CTC AAG CAC GCG GCG GTT GTT TAC GGA TTT CCA	480
Lys Glu Arg Gly Glu Leu Lys His Ala Ala Val Val Tyr Gly Phe Pro	
145 150 155 160	
TCA AGA AGC AGG AGG GAT ATA TCT CTT TAC CTG AAT GTG TTT AAA GAG	528
Ser Arg Ser Arg Arg Asp Ile Ser Leu Tyr Leu Asn Val Phe Lys Glu	
165 170 175	
GTC TTT TAC GAA GTA GGT TCC GTT AGG AGG CCC GGG GCC GCA GCG GTT	576
Val Phe Tyr Glu Val Gly Ser Val Arg Arg Pro Gly Ala Ala Val	
180 185 190	

GAT ATA TGC ATG CTT GCG GAG GGC ATA TTT GAC GGG ATG ATG GAG TTT	624
Asp Ile Cys Met Leu Ala Glu Gly Ile Phe Asp Gly Met Met Glu Phe	
195 200 205	
GAG ATG AAG CCA TGG GAC ATA ACG GCG GGA CTC GTA ATA CTG AAG GAA	672
Glu Met Lys Pro Trp Asp Ile Thr Ala Gly Leu Val Ile Leu Lys Glu	
210 215 220	
GCT GGA GGA TTT TAC ACA CTG AAG GGA GAC CCC TTC GGC ATC TCG GAC	720
Ala Gly Gly Phe Tyr Thr Leu Lys Gly Asp Pro Phe Gly Ile Ser Asp	
225 230 235 240	
ATA ATA GCG GGA AAC AGG ATG CTC CAC GAC TTC ATT CTC AAG GTT GTG	768
Ile Ile Ala Gly Asn Arg Met Leu His Asp Phe Ile Leu Lys Val Val	
245 250 255	
AAT AAA TAC ATG AAT AAT GAA AGC ACG	795
Asn Lys Tyr Met Asn Asn Glu Ser Thr	
260 265	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Glu	Asn	Leu	Glu	Lys	Leu	Leu	Glu	Val	Ala	Lys	Met	Ala	Ala	Leu
1				5					10					15	
Ala	Gly	Gly	Gln	Val	Leu	Lys	Glu	Asn	Phe	Gly	Lys	Ile	Lys	Leu	Glu
			20					25					30		
Asn	Ile	Glu	Glu	Lys	Gly	Glu	Lys	Asp	Phe	Val	Ser	Tyr	Val	Asp	Lys
		35					40					45			
Thr	Ser	Glu	Glu	Arg	Ile	Lys	Glu	Leu	Ile	Leu	Lys	Phe	Phe	Pro	Asp
	50					55					60				
His	Glu	Val	Val	Gly	Glu	Glu	Arg	Gly	Lys	Glu	Gly	Lys	Glu	Ser	Pro
	65				70				75					80	
Tyr	Lys	Trp	Phe	Ile	Asp	Pro	Leu	Asp	Gly	Thr	Lys	Asn	Tyr	Ile	Lys
			85						90					95	
Gly	Phe	Pro	Ile	Phe	Ala	Val	Ser	Val	Gly	Leu	Val	Lys	Glu	Asn	Glu
		100						105				110			
Pro	Ile	Val	Gly	Ala	Val	Tyr	Leu	Pro	Tyr	Phe	Asp	Thr	Leu	Tyr	Trp
	115						120				125				
Ala	Ser	Lys	Gly	Arg	Gly	Ala	Tyr	Lys	Asn	Gly	Glu	Arg	Ile	Ser	Val
	130					135				140					
Lys	Glu	Arg	Gly	Glu	Leu	Lys	His	Ala	Ala	Val	Val	Tyr	Gly	Phe	Pro
	145				150				155					160	
Ser	Arg	Ser	Arg	Arg	Asp	Ile	Ser	Leu	Tyr	Leu	Asn	Val	Phe	Lys	Glu
			165						170					175	
Val	Phe	Tyr	Glu	Val	Gly	Ser	Val	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Val
		180					185					190			
Asp	Ile	Cys	Met	Leu	Ala	Glu	Gly	Ile	Phe	Asp	Gly	Met	Met	Glu	Phe
	195					200					205				
Glu	Met	Lys	Pro	Trp	Asp	Ile	Thr	Ala	Gly	Leu	Val	Ile	Leu	Lys	Glu
	210				215						220				
Ala	Gly	Gly	Phe	Tyr	Thr	Leu	Lys	Gly	Asp	Pro	Phe	Gly	Ile	Ser	Asp
	225				230				235					240	
Ile	Ile	Ala	Gly	Asn	Arg	Met	Leu	His	Asp	Phe	Ile	Leu	Lys	Val	Val
			245					250						255	

Asn Lys Tyr Met Asn Asn Glu Ser Thr
260 265

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATG AGT GAA CAG CCG GTA TTG TCT GTT CAA GGA TTA AGC GGC GGG TAT	48
Met Ser Glu Gln Pro Val Leu Ser Val Gln Gly Leu Ser Gly Gly Tyr	
1 5 10 15	
AGC ATG AAC CGA CCG GTT CTG CAT GAC GTA ACC TTT CAG GTT GAA CCG	96
Ser Met Asn Arg Pro Val Leu His Asp Val Thr Phe Gln Val Glu Pro	
20 25 30	
GGT GAG ATG GTG GGT TTG ATC GGC CTG AAC GGT GCG GGC AAG AGT ACC	144
Gly Glu Met Val Gly Leu Ile Gly Leu Asn Gly Ala Gly Lys Ser Thr	
35 40 45	
ACG ATG AAG CAT ATT CTC GGG CTG ATG AAT CCG CAA AAA GGG AGC ATT	192
Thr Met Lys His Ile Leu Gly Leu Met Asn Pro Gln Lys Gly Ser Ile	
50 55 60	
CAG GTT CAA GGA AAG AGC CGG ACA GAG CAT TCG GAA GCC TAT CAC GGC	240
Gln Val Gln Gly Lys Ser Arg Thr Glu His Ser Glu Ala Tyr His Gly	
65 70 75 80	
GCC TTG GCG TTT GTT CCC GAA TCC CCG CTG CTG TAT GAG GAG ATG ACA	288
Ala Leu Ala Phe Val Pro Glu Ser Pro Leu Leu Tyr Glu Glu Met Thr	
85 90 95	
GTA CGA GAG CAT CTG GAA TTT ACG GCG CGC TCC TAT GGC GTA TCC CGT	336
Val Arg Glu His Leu Glu Phe Thr Ala Arg Ser Tyr Gly Val Ser Arg	
100 105 110	
GAA GAT TAT GAG GCA CGT TCG GAG CAG CTG TCG AAG ATG TTC CGT ATG	384
Glu Asp Tyr Glu Ala Arg Ser Glu Gln Leu Ser Lys Met Phe Arg Met	
115 120 125	
GAA GAG AAG ATG GAC AGC CTG TCC ACG CAT TTG TCC AAA GGG ATG CGC	432
Glu Glu Lys Met Asp Ser Leu Ser Thr His Leu Ser Lys Gly Met Arg	
130 135 140	
CAA AAA GTG ATG ATC ATG TGC GCA TTC GTA GCC AGA CCG TCC CTG TAC	480
Gln Lys Val Met Ile Met Cys Ala Phe Val Ala Arg Pro Ser Leu Tyr	
145 150 155 160	
ATC ATT GAC GAG CCC TTT CTT GGG CTT GAT CCG CTT GGG ATA CGC TCG	528
Ile Ile Asp Glu Pro Phe Leu Gly Leu Asp Pro Leu Gly Ile Arg Ser	
165 170 175	
CTG CTT GAC TTC ATG CTG GAG CTG AAG GCA TCC GGC GCT TCG GTA TTG	576
Leu Leu Asp Phe Met Leu Glu Leu Lys Ala Ser Gly Ala Ser Val Leu	

180

185

190

CTA AGC TCC CAC ATT
 Leu Ser Ser His Ile
 195

591

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ser	Glu	Gln	Pro	Val	Leu	Ser	Val	Gln	Gly	Leu	Ser	Gly	Gly	Tyr
1				5					10					15	
Ser	Met	Asn	Arg	Pro	Val	Leu	His	Asp	Val	Thr	Phe	Gln	Val	Glu	Pro
		20						25					30		
Gly	Glu	Met	Val	Gly	Leu	Ile	Gly	Leu	Asn	Gly	Ala	Gly	Lys	Ser	Thr
		35					40					45			
Thr	Met	Lys	His	Ile	Leu	Gly	Leu	Met	Asn	Pro	Gln	Lys	Gly	Ser	Ile
	50					55				60					
Gln	Val	Gln	Gly	Lys	Ser	Arg	Thr	Glu	His	Ser	Glu	Ala	Tyr	His	Gly
	65			70					75					80	
Ala	Leu	Ala	Phe	Val	Pro	Glu	Ser	Pro	Leu	Leu	Tyr	Glu	Glu	Met	Thr
			85					90						95	
Val	Arg	Glu	His	Leu	Glu	Phe	Thr	Ala	Arg	Ser	Tyr	Gly	Val	Ser	Arg
		100					105					110			
Glu	Asp	Tyr	Glu	Ala	Arg	Ser	Glu	Gln	Leu	Ser	Lys	Met	Phe	Arg	Met
		115				120					125				
Glu	Glu	Lys	Met	Asp	Ser	Leu	Ser	Thr	His	Leu	Ser	Lys	Gly	Met	Arg
	130					135					140				
Gln	Lys	Val	Met	Ile	Met	Cys	Ala	Phe	Val	Ala	Arg	Pro	Ser	Leu	Tyr
	145			150					155					160	
Ile	Ile	Asp	Glu	Pro	Phe	Leu	Gly	Leu	Asp	Pro	Leu	Gly	Ile	Arg	Ser
		165					170						175		
Leu	Leu	Asp	Phe	Met	Leu	Glu	Leu	Lys	Ala	Ser	Gly	Ala	Ser	Val	Leu
		180					185						190		
Leu	Ser	Ser	His	Ile											
		195													

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATG	AAG	AAA	ATA	ACT	ATT	AGT	AGT	TTG	CTT	CTA	CTT	TTA	CTT	ATT	TCT
Met	Lys	Lys	Ile	Thr	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Leu	Ile	Ser	
1				5				10					15		

48

ACC AAT TTG AAT CTC GCA TAC GAT TCC CAA GAG AGC GGT ATT AAA AAT	96
Thr Asn Leu Asn Leu Ala Tyr Asp Ser Gln Glu Ser Gly Ile Lys Asn	
20 25 30	
ATA ATA ATC CTC ATT GGA GAC GGC ATG GGA ATG AGT CAT GTC CAG ATT	144
Ile Ile Ile Leu Ile Gly Asp Gly Met Gly Met Ser His Val Gln Ile	
35 40 45	
ACA AAG CTT GTT TAT GGT CAT CTA AAC ATG GAA GAG TTC CCA ATT ATT	192
Thr Lys Leu Val Tyr Gly His Leu Asn Met Glu Glu Phe Pro Ile Ile	
50 55 60	
GGA TTC GAA CTT ACT GAG TCA TTA AGT GGG GAA GTT ACG GAC TCC GCT	240
Gly Phe Glu Leu Thr Glu Ser Leu Ser Gly Glu Val Thr Asp Ser Ala	
65 70 75 80	
GCA GCA GGA ACT GCA ATA GCA ACT GGA GTC AAA ACA TAT AAT CGA ATG	288
Ala Ala Gly Thr Ala Ile Ala Thr Gly Val Lys Thr Tyr Asn Arg Met	
85 90 95	
ATT TCA GTT ACT AAC ATA ACT GGA AAA GTT ACA AAT CTA ACT ACC TTG	336
Ile Ser Val Thr Asn Ile Thr Gly Lys Val Thr Asn Leu Thr Thr Leu	
100 105 110	
CTT GAA ATA GCC CAG GTA CTT GGA AAA TCA ACT GGA CTT GTG ACT ACT	384
Leu Glu Ile Ala Gln Val Leu Gly Lys Ser Thr Gly Leu Val Thr Thr	
115 120 125	
ACT AGA ATT ACA CAC GCA ACC CCT GCA GTA TTT GCT TCC CAC GTT CCT	432
Thr Arg Ile Thr His Ala Thr Pro Ala Val Phe Ala Ser His Val Pro	
130 135 140	
GAC AGA GAT ATG GAA GAG GAA ATA GCG AGA CAG CTC ATA GCT CAC CGG	480
Asp Arg Asp Met Glu Glu Glu Ile Ala Arg Gln Leu Ile Ala His Arg	
145 150 155 160	
GTC AAC GTC CTA TTA GGT GGA GGG AGA AAG AAA TTT GAC GAG AAT ACC	528
Val Asn Val Leu Leu Gly Gly Gly Arg Lys Lys Phe Asp Glu Asn Thr	
165 170 175	
CTA AAA ATG GCA AAA GAA CAG GGA TAT AAT ATA GTC TTC ACG AAA GAA	576
Leu Lys Met Ala Lys Glu Gln Gly Tyr Asn Ile Val Phe Thr Lys Glu	
180 185 190	
GAG CTC GAG AAA GCA GAG GGT GAG TTT ATT CTA GGG CTT TTT GCA GAT	624
Glu Leu Glu Lys Ala Glu Gly Glu Phe Ile Leu Gly Leu Phe Ala Asp	
195 200 205	
AGC CAC ATT CCT TAC GTA TTG GAC AGA AAA CCA GAA GAT GTT GGA CTT	672
Ser His Ile Pro Tyr Val Leu Asp Arg Lys Pro Glu Asp Val Gly Leu	
210 215 220	
TTG GAA ATG ACT AAA AAA GCA ATT TCA ATA CTA GAG AAA AAT CCA AAT	720
Leu Glu Met Thr Lys Lys Ala Ile Ser Ile Leu Glu Lys Asn Pro Asn	
225 230 235 240	
GGG TTC TTT CTC ATG ATT GAA GGG GGC AGA ATT GAT CAT GCA GCT CAT	768
Gly Phe Phe Leu Met Ile Glu Gly Gly Arg Ile Asp His Ala Ala His	
245 250 255	
GAG AAT GAT ATA GCA TCA GTT GTT GCA GAG ACT AAG GAG TTT GAT GAC	816
Glu Asn Asp Ile Ala Ser Val Val Ala Glu Thr Lys Glu Phe Asp Asp	
260 265 270	

GTT GTT GGA TAT GTT CTT GAG TAT GCA AAA AAG AGG GGA GAT ACA CTA Val Val Gly Tyr Val Leu Glu Tyr Ala Lys Lys Arg Gly Asp Thr Leu 275 280 285	864
GTA ATA GTG CTG GCT GAC CAT GAG ACA GGG GGG CTT GGA TTA GGT CTA Val Ile Val Leu Ala Asp His Glu Thr Gly Gly Leu Gly Leu Gly Leu 290 295 300	912
ACA TAT GGA GAT GCA ATT AAT GAA GAT GTC ATC AGG AAC ATA AAC GCT Thr Tyr Gly Asp Ala Ile Asn Glu Asp Val Ile Arg Asn Ile Asn Ala 305 310 315 320	960
AGT GTG TCG AAA ATT GCT AGT GAA ATA AGG GCA ACG AAT GAC ATA AAG Ser Val Ser Lys Ile Ala Ser Glu Ile Arg Ala Thr Asn Asp Ile Lys 325 330 335	1008
AGA GTT ATC AAA AAA TAT ACT GGA TTC GAG CTA ACA GAG GAC GAA ATT Arg Val Ile Lys Lys Tyr Thr Gly Phe Glu Leu Thr Glu Asp Glu Ile 340 345 350	1056
AAT TAC ATT GAG GAA GCT ATA AAC TTA GCA GAC GAA TAT GCG CTT CAA Asn Tyr Ile Glu Glu Ala Ile Asn Leu Ala Asp Glu Tyr Ala Leu Gln 355 360 365	1104
AAT GCA ATA GCT GAT ATT ATA AAC AAA CGC GTT GGT GTA GGT TTT GTA Asn Ala Ile Ala Asp Ile Ile Asn Lys Arg Val Gly Val Gly Phe Val 370 375 380	1152
TCC CAC AAA CAT ACA GGA GCT CCT GTT TCA CTT CTA GCC TAC GGC CCA Ser His Lys His Thr Gly Ala Pro Val Ser Leu Leu Ala Tyr Gly Pro 385 390 395 400	1200
GGT GCA GAG AAT TTT GCA GGC TTT TTA CAC CAT GTA GAT ACG GCA AAG Gly Ala Glu Asn Phe Ala Gly Phe Leu His His Val Asp Thr Ala Lys 405 410 415	1248
CTA ATT GCC AAG CTA ATG CTC TTT GGG AAG AAA GAT ATT CCC GTT ACC Leu Ile Ala Lys Leu Met Leu Phe Gly Lys Lys Asp Ile Pro Val Thr 420 425 430	1296
ATC TTG GGA ATA AGT GGA GTT AAA GGA GAT ATA ACC GGA GAC TTC AAA Ile Leu Gly Ile Ser Gly Val Lys Gly Asp Ile Thr Gly Asp Phe Lys 435 440 445	1344
GTG GAT GAG CAA GAT GCA TAT GTG ACC TTA ATG ATG TTG CTT GGG GAA Val Asp Glu Gln Asp Ala Tyr Val Thr Leu Met Met Leu Leu Gly Glu 450 455 460	1392
AGG GTA GAT ACT GAA CTT GAA AGG AAA GTC GAC ATG AAT AAT AAC GGC Arg Val Asp Thr Glu Leu Glu Arg Lys Val Asp Met Asn Asn Asn Gly 465 470 475 480	1440
ATA ATC GAG TTG GGA GAC GTG CTC CTG ATT CTA CAA GAG TCC Ile Ile Glu Leu Gly Asp Val Leu Leu Ile Leu Gln Glu Ser 485 490	1482

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Lys	Ile	Thr	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Ile	Ser
1				5				10						15	
Thr	Asn	Leu	Asn	Leu	Ala	Tyr	Asp	Ser	Gln	Glu	Ser	Gly	Ile	Lys	Asn
			20					25					30		
Ile	Ile	Ile	Leu	Ile	Gly	Asp	Gly	Met	Gly	Met	Ser	His	Val	Gln	Ile
		35					40					45			
Thr	Lys	Leu	Val	Tyr	Gly	His	Leu	Asn	Met	Glu	Glu	Phe	Pro	Ile	Ile
	50					55				60					
Gly	Phe	Glu	Leu	Thr	Glu	Ser	Leu	Ser	Gly	Glu	Val	Thr	Asp	Ser	Ala
65					70					75					80
Ala	Ala	Gly	Thr	Ala	Ile	Ala	Thr	Gly	Val	Lys	Thr	Tyr	Asn	Arg	Met
				85					90					95	
Ile	Ser	Val	Thr	Asn	Ile	Thr	Gly	Lys	Val	Thr	Asn	Leu	Thr	Thr	Leu
			100					105					110		
Leu	Glu	Ile	Ala	Gln	Val	Leu	Gly	Lys	Ser	Thr	Gly	Leu	Val	Thr	Thr
		115					120					125			
Thr	Arg	Ile	Thr	His	Ala	Thr	Pro	Ala	Val	Phe	Ala	Ser	His	Val	Pro
	130					135				140					
Asp	Arg	Asp	Met	Glu	Glu	Ile	Ala	Arg	Gln	Leu	Ile	Ala	His	Arg	
145					150				155					160	
Val	Asn	Val	Leu	Leu	Gly	Gly	Gly	Arg	Lys	Lys	Phe	Asp	Glu	Asn	Thr
				165					170					175	
Leu	Lys	Met	Ala	Lys	Glu	Gln	Gly	Tyr	Asn	Ile	Val	Phe	Thr	Lys	Glu
		180						185					190		
Glu	Leu	Glu	Lys	Ala	Glu	Gly	Glu	Phe	Ile	Leu	Gly	Leu	Phe	Ala	Asp
		195					200					205			
Ser	His	Ile	Pro	Tyr	Val	Leu	Asp	Arg	Lys	Pro	Glu	Asp	Val	Gly	Leu
	210					215				220					
Leu	Glu	Met	Thr	Lys	Lys	Ala	Ile	Ser	Ile	Leu	Glu	Lys	Asn	Pro	Asn
225					230					235				240	
Gly	Phe	Phe	Leu	Met	Ile	Glu	Gly	Gly	Arg	Ile	Asp	His	Ala	Ala	His
				245					250					255	
Glu	Asn	Asp	Ile	Ala	Ser	Val	Val	Ala	Glu	Thr	Lys	Glu	Phe	Asp	Asp
			260					265					270		
Val	Val	Gly	Tyr	Val	Leu	Glu	Tyr	Ala	Lys	Lys	Arg	Gly	Asp	Thr	Leu
		275					280					285			
Val	Ile	Val	Leu	Ala	Asp	His	Glu	Thr	Gly	Gly	Leu	Gly	Leu	Gly	Leu
	290					295					300				
Thr	Tyr	Gly	Asp	Ala	Ile	Asn	Glu	Asp	Val	Ile	Arg	Asn	Ile	Asn	Ala
305					310					315				320	
Ser	Val	Ser	Lys	Ile	Ala	Ser	Glu	Ile	Arg	Ala	Thr	Asn	Asp	Ile	Lys
				325					330					335	
Arg	Val	Ile	Lys	Lys	Tyr	Thr	Gly	Phe	Glu	Leu	Thr	Glu	Asp	Glu	Ile
			340					345					350		
Asn	Tyr	Ile	Glu	Glu	Ala	Ile	Asn	Leu	Ala	Asp	Glu	Tyr	Ala	Leu	Gln
		355					360					365			
Asn	Ala	Ile	Ala	Asp	Ile	Ile	Asn	Lys	Arg	Val	Gly	Val	Gly	Phe	Val
		370				375					380				
Ser	His	Lys	His	Thr	Gly	Ala	Pro	Val	Ser	Leu	Leu	Ala	Tyr	Gly	Pro
385					390					395				400	
Gly	Ala	Glu	Asn	Phe	Ala	Gly	Phe	Leu	His	His	Val	Asp	Thr	Ala	Lys
				405					410					415	
Leu	Ile	Ala	Lys	Leu	Met	Leu	Phe	Gly	Lys	Lys	Asp	Ile	Pro	Val	Thr
			420					425					430		
Ile	Leu	Gly	Ile	Ser	Gly	Val	Lys	Gly	Asp	Ile	Thr	Gly	Asp	Phe	Lys
		435					440					445			
Val	Asp	Glu	Gln	Asp	Ala	Tyr	Val	Thr	Leu	Met	Met	Leu	Leu	Gly	Glu
	450					455					460				
Arg	Val	Asp	Thr	Glu	Leu	Glu	Arg	Lys	Val	Asp	Met	Asn	Asn	Asn	Gly
465					470					475					480
Ile	Ile	Glu	Leu	Gly	Asp	Val	Leu	Leu	Ile	Leu	Gln	Glu	Ser		

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATG	ATT	AAC	CAA	ATA	AAC	TTC	AAA	ACC	TCT	CAT	GGA	GGA	AGC	AGA	GAA	48
Met	Ile	Asn	Gln	Ile	Asn	Phe	Lys	Thr	Ser	His	Gly	Gly	Ser	Arg	Glu	
1				5					10					15		
GAA	GGC	TAC	ATA	AAC	TTC	TCG	GCC	TCT	GTA	AAT	CCT	TAT	CCA	CCA	GAA	96
Glu	Gly	Tyr	Ile	Asn	Phe	Ser	Ala	Ser	Val	Asn	Pro	Tyr	Pro	Pro	Glu	
			20					25					30			
TGG	ACT	GAT	GAA	ATG	TTT	GAG	AGG	GCT	AAA	AAG	ATA	AGC	ACC	TTC	TAT	144
Trp	Thr	Asp	Glu	Met	Phe	Glu	Arg	Ala	Lys	Lys	Ile	Ser	Thr	Phe	Tyr	
		35					40					45				
CCT	TAC	TAT	GAA	AAG	CTT	GAG	GAA	GAA	CTC	TCA	GAT	CTA	ATT	GGG	GAG	192
Pro	Tyr	Tyr	Glu	Lys	Leu	Glu	Glu	Glu	Leu	Ser	Asp	Leu	Ile	Gly	Glu	
	50					55					60					
CCA	ATA	ACT	ATA	ACT	GCA	GGA	ATA	ACA	GAG	GCA	CTT	TAC	CTG	CTT	GGA	240
Pro	Ile	Thr	Ile	Thr	Ala	Gly	Ile	Thr	Glu	Ala	Leu	Tyr	Leu	Leu	Gly	
65					70				75						80	
GTT	TGG	ATG	AGG	GGT	CGG	AAA	GTA	ATA	ATC	CCG	AAG	CAC	ACC	TAT	GGG	288
Val	Trp	Met	Arg	Gly	Arg	Lys	Val	Ile	Ile	Pro	Lys	His	Thr	Tyr	Gly	
				85					90					95		
GAA	TAC	GAG	AGG	ATC	TCA	CGC	ATG	TTC	GGA	GGT	AGG	GTG	ATC	AAA	GGT	336
Glu	Tyr	Glu	Arg	Ile	Ser	Arg	Met	Phe	Gly	Gly	Arg	Val	Ile	Lys	Gly	
			100					105					110			
CCC	AAT	GAC	CCA	GGA	AAG	TTA	GCA	GAA	TTT	GTT	GAA	AGA	AAT	TCA	TTC	384
Pro	Asn	Asp	Pro	Gly	Lys	Leu	Ala	Glu	Phe	Val	Glu	Arg	Asn	Ser	Phe	
		115					120					125				
GTG	TTC	TTC	TGC	AAT	CCA	AAC	AAT	CCA	GAT	GGA	AAG	TTC	TAC	CGA	GAA	432
Val	Phe	Phe	Cys	Asn	Pro	Asn	Asn	Pro	Asp	Gly	Lys	Phe	Tyr	Arg	Glu	
	130					135					140					
AAA	GAG	ATG	AAA	CCT	CTT	TTA	GAT	GCC	ATT	CAA	GAC	ACT	AAC	TCA	ATT	480
Lys	Glu	Met	Lys	Pro	Leu	Leu	Asp	Ala	Ile	Gln	Asp	Thr	Asn	Ser	Ile	
145					150					155					160	
TTG	ATC	TTG	GAT	GAA	GCC	TTC	ATA	GAC	TTT	GTT	AAG	AAA	CCA	GAA	AGC	528
Leu	Ile	Leu	Asp	Glu	Ala	Phe	Ile	Asp	Phe	Val	Lys	Lys	Pro	Glu	Ser	
				165					170					175		
CCA	GAG	GGA	GAG	AAC	ATA	ATC	AGG	CTA	AGG	ACT	TTT	ACC	AAA	AGC	TAC	576
Pro	Glu	Gly	Glu	Asn	Ile	Ile	Arg	Leu	Arg	Thr	Phe	Thr	Lys	Ser	Tyr	
			180					185					190			

GGG CTC CCA GGG GTA AGG GTT GGA TAT GTT ATT GGA TTT GTC GAT GCT	624
Gly Leu Pro Gly Val Arg Val Gly Tyr Val Ile Gly Phe Val Asp Ala	
195 200 205	
TTC AGG AGC GTT AGA ATG CCA TGG TCA ATT GGC TCT ACT GGG GTG GCC	672
Phe Arg Ser Val Arg Met Pro Trp Ser Ile Gly Ser Thr Gly Val Ala	
210 215 220	
TTC TTA GAG TTC TTA CTC AAA GAT AAC TTC AAA CAC TTA AGA AAA ACC	720
Phe Leu Glu Phe Leu Leu Lys Asp Asn Phe Lys His Leu Arg Lys Thr	
225 230 235 240	
CTC CCC CTA ATA TGG AAA GAA AAG GAG AGG ATT GAG AAA GAA TTG AAA	768
Leu Pro Leu Ile Trp Lys Glu Lys Glu Arg Ile Glu Lys Glu Leu Lys	
245 250 255	
GTT AAA AGC GAT GCA AAT TTC TTC ATT ATG AAG GTC AGA GAA GGA ATA	816
Val Lys Ser Asp Ala Asn Phe Phe Ile Met Lys Val Arg Glu Gly Ile	
260 265 270	
ATT GAA AAG CTA AAA GAG AAT GGC ATC CTT GTA AGG GAT TGC AAG AGC	864
Ile Glu Lys Leu Lys Glu Asn Gly Ile Leu Val Arg Asp Cys Lys Ser	
275 280 285	
TTT GGA CTC CCT GGG TAC ATA AGG TTT TCA GTT AGA AGG AGA GAA GAG	912
Phe Gly Leu Pro Gly Tyr Ile Arg Phe Ser Val Arg Arg Arg Glu Glu	
290 295 300	
AAT GAC AAA CTC ATA AAC ATC CTT AGA AAA ACA CTT AAT ACT	954
Asn Asp Lys Leu Ile Asn Ile Leu Arg Lys Thr Leu Asn Thr	
305 310 315	

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ile	Asn	Gln	Ile	Asn	Phe	Lys	Thr	Ser	His	Gly	Gly	Ser	Arg	Glu
1				5					10					15	
Glu	Gly	Tyr	Ile	Asn	Phe	Ser	Ala	Ser	Val	Asn	Pro	Tyr	Pro	Pro	Glu
			20					25					30		
Trp	Thr	Asp	Glu	Met	Phe	Glu	Arg	Ala	Lys	Lys	Ile	Ser	Thr	Phe	Tyr
		35					40					45			
Pro	Tyr	Tyr	Glu	Lys	Leu	Glu	Glu	Glu	Leu	Ser	Asp	Leu	Ile	Gly	Glu
	50					55					60				
Pro	Ile	Thr	Ile	Thr	Ala	Gly	Ile	Thr	Glu	Ala	Leu	Tyr	Leu	Leu	Gly
	65				70				75					80	
Val	Trp	Met	Arg	Gly	Arg	Lys	Val	Ile	Ile	Pro	Lys	His	Thr	Tyr	Gly
				85				90						95	
Glu	Tyr	Glu	Arg	Ile	Ser	Arg	Met	Phe	Gly	Gly	Arg	Val	Ile	Lys	Gly
			100					105					110		
Pro	Asn	Asp	Pro	Gly	Lys	Leu	Ala	Glu	Phe	Val	Glu	Arg	Asn	Ser	Phe
		115					120					125			
Val	Phe	Phe	Cys	Asn	Pro	Asn	Asn	Pro	Asp	Gly	Lys	Phe	Tyr	Arg	Glu
	130					135					140				
Lys	Glu	Met	Lys	Pro	Leu	Leu	Asp	Ala	Ile	Gln	Asp	Thr	Asn	Ser	Ile

145					150					155				160
Leu	Ile	Leu	Asp	Glu	Ala	Phe	Ile	Asp	Phe	Val	Lys	Lys	Pro	Glu
				165					170					175
Pro	Glu	Gly	Glu	Asn	Ile	Ile	Arg	Leu	Arg	Thr	Phe	Thr	Lys	Ser
			180					185					190	
Gly	Leu	Pro	Gly	Val	Arg	Val	Gly	Tyr	Val	Ile	Gly	Phe	Val	Asp
		195					200				205			Ala
Phe	Arg	Ser	Val	Arg	Met	Pro	Trp	Ser	Ile	Gly	Ser	Thr	Gly	Val
	210					215					220			Ala
Phe	Leu	Glu	Phe	Leu	Leu	Lys	Asp	Asn	Phe	Lys	His	Leu	Arg	Lys
225				230						235				240
Leu	Pro	Leu	Ile	Trp	Lys	Glu	Lys	Glu	Arg	Ile	Glu	Lys	Glu	Leu
			245						250					255
Val	Lys	Ser	Asp	Ala	Asn	Phe	Phe	Ile	Met	Lys	Val	Arg	Glu	Gly
			260					265					270	Ile
Ile	Glu	Lys	Leu	Lys	Glu	Asn	Gly	Ile	Leu	Val	Arg	Asp	Cys	Lys
		275				280						285		Ser
Phe	Gly	Leu	Pro	Gly	Tyr	Ile	Arg	Phe	Ser	Val	Arg	Arg	Arg	Glu
	290					295				300				Glu
Asn	Asp	Lys	Leu	Ile	Asn	Ile	Leu	Arg	Lys	Thr	Leu	Asn	Thr	
305					310					315				

Q2
Concluded